

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:25:16 ; Search time 7.60425 Seconds
(without alignments)
661.194 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110

Perfect score: 78

Sequence: 1 AYGWQDIYSL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	478	2 AAR46065	Aar46065 Mutant al
2	78	100.0	478	2 AAR72450	Aar72450 Aspergill
3	78	100.0	478	2 AAR78270	Aar78270 Aspergill
4	78	100.0	478	2 AAW14500	Aaw14500 Aspergill
5	78	100.0	498	4 AAB84206	Aab84206 Amino aci
6	78	100.0	498	8 ADT89632	Adt89632 Aspergill
7	78	100.0	499	8 ADT89628	Adt89628 Aspergill
8	78	100.0	1095	6 ABP96630	Abp96630 Alpha-amy
9	75	96.2	495	6 ABB80177	Abb80177 A. fumiga
10	70	89.7	423	4 ABB09072	Abb09072 Aspergill
11	70	89.7	494	6 ABP97894	Abp97894 Amino aci
12	69	88.5	55	2 AAR88213	Aar88213 Alpha-amy
13	69	88.5	493	2 AAR88212	Aar88212 Alpha-amy
14	69	88.5	500	8 ADS23436	Ads23436 Bacterial
15	67	85.9	513	8 ADN19570	Adn19570 Bacterial
16	65	83.3	547	6 ABB80179	Abb80179 A. fumiga
17	64	82.1	484	5 AAE24207	Aae24207 Aspergill
18	64	82.1	484	8 ADS75939	Ads75939 Aspergill
19	63	80.8	555	6 ABP97896	Abp97896 Amino aci
20	63	80.8	567	6 ABP97899	Abp97899 Amino aci
21	62	79.5	478	2 AAR79025	Aar79025 Mature ta
22	58	74.4	468	2 AAR24136	Aar24136 Alpha-amy
23	58	74.4	494	1 AAP70571	Aap70571 Alpha-amy
24	58	74.4	630	6 ABB80178	Abb80178 A. fumiga
25	57	73.1	549	6 ABP97895	Abp97895 Amino aci

26	56	71.8	493	8 ADS44293	Ads44293 Bacterial
27	54	69.2	468	2 AAR63184	Aar63184 Variant a
28	53	67.9	468	2 AAR63185	Aar63185 Variant a
29	53	67.9	564	8 ADS44249	Ads44249 Bacterial
30	52	66.7	711	5 ADP26024	Adp26024 Streptoco
31	50	64.1	452	2 AAR63186	Aar63186 Variant a
32	50	64.1	511	1 AAP81161	Aap81161 Recombina
33	50	64.1	511	1 AAP81180	Aap81180 Sequence
34	50	64.1	512	2 AAR07574	Aar07574 Alpha-amy
35	49	62.8	468	2 AAR63187	Aar63187 Variant a
36	49	62.8	656	2 AAR06109	Aar06109 Sequence
37	49	62.8	686	1 AAP61518	Aap61518 Sequence
38	49	62.8	686	2 AAW17605	Aaw17605 Bacillus
39	49	62.8	686	2 AAW17600	Aaw17600 Bacillus
40	49	62.8	686	2 AAW17603	Aaw17603 Bacillus
41	49	62.8	686	2 AAW17592	Aaw17592 Bacillus
42	49	62.8	686	2 AAW17596	Aaw17596 Bacillus
43	49	62.8	686	2 AAW06773	Aaw06773 Wild type
44	49	62.8	686	2 AAW17599	Aaw17599 Bacillus
45	49	62.8	686	2 AAW17594	Aaw17594 Bacillus

ALIGNMENTS

RESULT 1

AAR46065
ID AAR46065 standard; protein; 478 AA.

XX AAR46065;

XX 25-MAR-2003 (revised)

DT 18-JUL-1994 (first entry)

XX Mutant alpha-amylase.

DE Methionine substitution; stability; activity; detergent;

XX dishwashing agents; liquifaction agents.

KW Aspergillus oryzae.

XX

OS

XX

PN

XX

XX

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SQ Sequence 478 AA;
Query Match 100.0%; Score 78; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
DB 78 AYHGYWQDIYSL 90

RESULT 2
AAR72450
ID AAR72450 standard; protein; 478 AA.
XX AC
XX AAR72450;
XX AC
XX 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)
XX DE
XX Aspergillus oryzae alpha amylase (mature protein).
XX XX
XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
KW thermostable.
XX XX
XX Aspergillus oryzae.
OS OS
XX WO9510603-A1.
XX PN
XX 20-APR-1995.
XX PD
XX 05-OCT-1994; 94WO-DK000370.
XX PF
XX 08-OCT-1993; 93DK-00001133.
XX PR
XX 02-FEB-1994; 94DK-0000140.
XX PR
XX (NOVO ) NOVO-NORDISK AS.
XX PA
XX Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;
XX PI
XX WPI; 1995-161790/21.
XX DR
XX New Bacillus derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
XX PT
XX Disclosure; Page 75-76; 105pp; English.
XX PS
XX Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability; low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
XX CC
XX SQ Sequence 478 AA;

Query Match 100.0%; Score 78; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
DB 78 AYHGYWQDIYSL 90

RESULT 3
AAR78270
ID AAR78270 standard; protein; 478 AA.
XX AC
XX AAR78270;
XX AC
XX 04-JUN-1997 (first entry)
XX DT
XX Aspergillus oryzae alpha-amylase (mature protein).
XX DE
XX alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
KW Aspergillus oryzae; Bacillus amyloliquefaciens; altered property;
KW calcium dependency; substrate binding; stability; pH optimum;
KW thermostability; cleavage; oligosaccharide substrate; dishwashing;
KW washing; detergent additive; fabric desizing; starch liquefaction;
KW sweetener; ethanol production; variant.
XX KW
XX Aspergillus oryzae.
OS OS

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FH Key Location/Qualifiers
FT Misc-difference 13..45
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 7-23 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 33"
FT
FT Misc-difference 14..40
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 8-18 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 35"
FT
FT Misc-difference 28..42
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT
FT Misc-difference 32..38
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 14-15 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 32"
FT
FT Misc-difference 66..84
FT /label= loop 2 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 44-57 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 18"
FT
FT Misc-difference 70..78
FT /label= loop 2 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 48-51 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 20"
FT
FT Misc-difference 98..120
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 117-185 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 24"
FT
FT Misc-difference 102..206
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 121-181 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 26"
FT
FT Misc-difference 121..181
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to this fragment is deleted or replaced with a fragment
FT corresponding to 102-206 of AAW14499; claim 41"
FT
FT Misc-difference 121..174
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to this fragment is deleted or
FT replaced with a fragment corresponding to 102-199 of
FT AAW14499; claim 42"
FT
FT Misc-difference 165..177
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 195-202 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 21"
FT
FT Misc-difference 166..173
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 196-198 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 23"
FT
FT Misc-difference 181..184
FT /note= "an amino acid fragment corresponding to this
FT region is deleted from the parent sequence of a variant
FT Fungamyl; claim 43"
FT
FT Misc-difference 291..313
FT /label= loop 8 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 322-346 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 36"
FT
FT Misc-difference 297..313
FT /label= loop 8 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 325-345 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 38"
FT
FT WO9623874-A1.
FT
FT 08-AUG-1996.
FT
FT 05-FEB-1996; 96WO-DK000057.
FT
FT 03-FEB-1995; 95DK-00000128.
FT
FT 23-OCT-1995; 95DK-00001192.
FT
FT 10-NOV-1995; 95DK-00001256.
FT
FT (NOVO ) NOVO-NORDISK AS.
FT
FT Svendsen A, Bisgaard-Frantzen H, Borchert TV;
FT WPI; 1996-371424/37.
FT
FT Alpha-amylase variants and methods of production - have altered
FT properties such as calcium dependency, substrate binding and stability.
FT
FT Disclosure; Page 87-88; 171pp; English.
FT
FT The present sequence is the mature Aspergillus oryzae alpha-amylase (A).
FT Variants of parent tetramyl- and fungamyl-like alpha-amylases (and
FT methods of constructing them) are claimed. Examples of variants are
FT featured above. The variants have altered properties such as calcium
FT dependency, substrate binding and stability. Also one or more proline or
FT cysteine residues in the variant is modified or replaced with a non-
FT proline or non-cysteine residue such as alanine. The variants can be used
FT for (dish)washing, as detergent additives or for fabric desizing or
FT starch liquefaction. They can also be used for the production of
FT sweeteners and ethanol from starch. See also AAW14498-99
FT
FT Sequence 478 AA;
FT
FT Query Match 100.0%; Score 78; DB 2; Length 478;
FT Best Local Similarity 100.0%; Pred. No. 0.0011;
FT Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT QY 1 AYHGYWQDIYSL 13
FT |||||
FT Db 78 AYHGYWQDIYSL 90
FT
FT RESULT 5
FT AAB84206
FT ID AAB84206 standard; protein; 498 AA.
FT XX
FT AAB84206;
FT AC
FT XX 06-AUG-2001 (first entry)
FT XX

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DE Amino acid sequence of a fungamyl-like alpha-amylase.
XX
KW Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
KW alcohol; starch; dough improver; brewing; starch liquification.
XX
OS Aspergillus oryzae.
XX
PN WO200134784-A1.
XX
PD 17-MAY-2001.
XX
XX 10-NOV-2000; 2000NO-DK000626.
PF
XX 10-NOV-1999; 99DK-00001617.
PR
XX (NOVO) NOVOZYMES AS.
PA
XX Bisgard-Frantzen H, Svendsen A, Pedersen S;
PI
XX WPI; 2001-367478/38.
DR N-PSDB; AAF90208.
DR
XX New variant of Fungamyl-like alpha-amylase, useful for production of
PT maltose syrups, includes mutations that improve stability against heat
PT and acidic pH.
PT
XX
PS Claim 1; Page 42-45; 49pp; English.
XX
XX The present sequence represents a fungamyl-like alpha-amylase. The
CC specification describes variants of this fungamyl-like alpha-amylase,
CC which have an alteration in one the amino acid regions 98-110, 150-160,
CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
CC substitution of an amino acid or an insertion of an amino acid downstream
CC of a particular position. The variants retain alpha-amylase activity, and
CC have better heat stability and/or stability at acidic pH, relative to
CC wild-type enzyme. The variants can therefore be used at higher
CC temperatures (more efficient conversion or faster reaction, and have
CC reduced need for cooling and reduced risk of contamination). The variants
CC may also be used in conjunction with other enzymes, particularly
CC glucoamylase during dextrinisation. The variants are used to produce
CC syrups, particularly of high maltose content, or alcohol, from starch; as
CC dough improver for baked goods; in brewing, to increase fermentability of
CC the wort; and for liquefaction of starch
XX
XX Sequence 498 AA;
SQ
Query Match 100.0%; Score 78; DB 4; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AYHGYWQDIYSL 13
DB 98 AYHGYWQDIYSL 110
RESULT 6
ADT89632
ID ADT89632 standard; protein; 498 AA.
XX
AC ADT89632;
XX
XX 16-DEC-2004 (first entry)
DT
XX Aspergillus niger neutral alpha-amylase A (amyA) protein.
DE
XX Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.
KW
XX Aspergillus niger.
OS
XX US2004191864-A1.
PN
XX 30-SEP-2004.
PD
XX

PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
XX (NOVO) NOVOZYMES BIOTECH INC.
PA
XX Connelly M, Brody H;
PI
XX WPI; 2004-708545/69.
DR N-PSDB; ADT89631.
DR
XX Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
PT
XX
XX Example 11; SEQ ID NO 22; 59pp; English.
PS
XX The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
XX Sequence 498 AA;
SQ
Query Match 100.0%; Score 78; DB 8; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AYHGYWQDIYSL 13
DB 99 AYHGYWQDIYSL 111
RESULT 7
ADT89628
ID ADT89628 standard; protein; 499 AA.
XX
AC ADT89628;
XX
XX 16-DEC-2004 (first entry)
DT
XX Aspergillus niger neutral alpha-amylase B (amyB) protein.
DE
XX Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
KW
XX Aspergillus niger.
OS
XX US2004191864-A1.
PN
XX 30-SEP-2004.
PD
XX 31-MAR-2004; 2004US-00815495.
PF
XX 31-MAR-2003; 2003US-0459902P.
PR
XX (NOVO) NOVOZYMES BIOTECH INC.
PA
XX Connelly M, Brody H;
PI
XX WPI; 2004-708545/69.
DR N-PSDB; ADT89627.
DR
XX Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
PT
XX
XX Example 10; SEQ ID NO 18; 58pp; English.
PS

XX The present invention relates to a method of producing heterologous
 CC biological substance. The method involves culturing mutant of wild-type
 CC *Aspergillus niger* strain in medium suitable for producing heterologous
 CC biological substance, where mutant strain comprises first nucleotide
 CC sequence encoding heterologous biological substance and second nucleotide
 CC sequences comprising modification of glucoamylase (glua) and recovering
 CC heterologous biological substance. The present sequence is the
 CC *Aspergillus niger* neutral alpha-amylase B (amyB) protein.
 XX

SQ Sequence 499 AA;
 Query Match 100.0%; Score 78; DB 8; Length 499;
 Best Local Similarity 100.0%; Pred. NO. 0.0011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
 |||||
 Db 99 AYHGYWQDIYSL 111

RESULT 8
 ABP96630
 ID ABP96630 standard; protein; 1095 AA.
 XX
 AC ABP96630;

XX 02-JUN-2003 (first entry)

DE Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.

XX Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
 KW pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
 KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
 KW maltodextrin; ethanol; fermentation; beverage; enzyme.
 XX

OS *Aspergillus shirousami*.
 OS Synthetic.

XX WO2003018766-A2.

XX 06-MAR-2003.

XX 27-AUG-2002; 2002WO-US027129.

XX 27-AUG-2001; 2001US-0315281P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Lanahan MB, Basu SS, Batie CJ, Chen W, Craig J, Kinkema M;

XX WPI; 2003-268420/26.

XX N-PSDB; ACC44572.

XX Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
 PT alpha-amylase, useful for producing plant to produce food products having
 PT improved taste or fermentable substrates for ethanol.

XX Claim 1; Page 107; 158pp; English.

XX The present invention describes polynucleotides which encode processing
 CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
 CC isomerase, or glucoamylase) that are optimised for expression in plants.
 CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
 CC processing enzymes, which are activated under suitable conditions to act
 CC upon the desired substrate. Also described are self-processing transgenic
 CC plants and plant parts, e.g. grain, which express one or more of these
 CC enzymes and have an altered composition that facilitates plant and grain
 CC processing. Also described is a method (M) for converting starch to
 CC starch-derived products in a transformed plant part (TPP), by activating
 CC the starch processing enzyme contained in it. Transgenic grain is useful
 CC for preparing maltodextrin. A transformed plant (TP) can be used to
 CC produce food products having improved taste and to produce fermentable

CC substrates for ethanol and fermented beverages. (M) eliminates the need
 CC to mill or physically disrupt the integrity of plant parts prior to
 CC recovery of starch-derived products. The present sequence represents
 CC alpha-amylase/glucoamylase fusion protein, which is given in the
 CC exemplification of the present invention
 XX

SQ Sequence 1095 AA;

Query Match 100.0%; Score 78; DB 6; Length 1095;
 Best Local Similarity 100.0%; Pred. NO. 0.0025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
 |||||
 Db 78 AYHGYWQDIYSL 90

RESULT 9
 ABB80177
 ID ABB80177 standard; protein; 495 AA.
 XX

XX ABB80177;

XX 11-AUG-2003 (first entry)

XX A. fumigatus AFAAL1.

XX Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
 KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
 KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
 KW glucose; oxygen; myo-inositol phosphate; laccase; tea leaf; sucrose;
 KW glyceride; starch; maltodextrin; oxidated phenolic compound;
 KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
 KW textile; tea liquor; cleaning ability.
 XX

OS *Aspergillus fumigatus*.

XX WO2003012071-A2.

XX 13-FEB-2003.

XX 05-AUG-2002; 2002WO-US024842.

XX 03-AUG-2001; 2001US-0309870P.

XX (ELIT-) ELITRA PHARM INC.

XX Jiang B, Storms R, Roemer T, Bussey H;

XX WPI; 2003-332729/31.

XX N-PSDB; ABQ80345, ABQ80346.

XX Novel isolated *Aspergillus fumigatus* polypeptide, useful in various
 PT industries such as those involved in the making of food and feed,
 PT beverages, textiles and detergents.

XX Claim 17; Page 134-35; 169pp; English.

XX The sequences given in ABB80164-87 show enzymatic proteins derived from
 CC A. fumigatus. These proteins display the catalytic activity of an enzyme
 CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
 CC galactosidase, invertase, lipase, alpha-amylase, laccase,
 CC polygalacturonase or xylanase. Compositions comprising the tannase are
 CC useful for modulating the amount of compounds that comprise a gallate
 CC ester linkage in a composition. Compositions comprising cellulase are
 CC useful for modulating the amount of cellulose in a composition.
 CC Compositions comprising glucose oxidase are useful for modulating the
 CC amount of glucose or oxygen in a composition. Compositions comprising
 CC phytase are useful for modulating the amount of myo-inositol phosphates
 CC in a composition. Compositions comprising beta-galactosidase are useful
 CC for modulating the amount of lactose in a composition. Compositions
 CC comprising sucrose or invertase are useful for modulating the amount of
 CC sucrose in a composition. Compositions comprising lipase are useful for

modulating the amount of glyceride in a composition. Compositions comprising alpha-amylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising laccases are useful for modulating the amount of oxidized phenolic compounds in a composition. Compositions comprising polygalacturonases are useful for modulating the amount of high or low molecular weight polygalacturonic acid chains in a composition. Compositions comprising xylanases are useful for modulating the amount of xylan or xylo-oligomers in a composition. The A. fumigatus proteins and corresponding DNA's are useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents. The DNA's are useful to express recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleotide sequence of A. fumigatus to identify duplicated genes of paralogs having the same or similar biochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify potential orthologous enzyme genes for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, and to raise anti-protein antibodies. The polypeptide having tannase activity increases the yield of tea liquor from tea leaves, improves the colour, flavour and health benefits of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions

XX SQ Sequence 495 AA;

Query Match 96.2%; Score 75; DB 6; Length 495;
Best Local Similarity 92.3%; Pred. No. 0.0032;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
| | | | | | | | | |
Db 97 AYHGYWQDIYSV 109

RESULT 10
ID ABB09072 standard; protein; 423 AA.
XX AC ABB09072;
XX DT 26-JUN-2002 (first entry)
XX DE Aspergillus oryzae TAKA protein (TAA).
XX KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
XX KM protein co-ordinate data; 3 dimensional structure.
XX OS Aspergillus oryzae.
XX PN KR2001027418-A.
XX PD 06-APR-2001.
XX PF 09-SEP-1999; 99KR-00039130.
XX PR 09-SEP-1999; 99KR-00039130.
XX PA (POST-) POSTECH FOUND.
XX PA (SAMY-) SAMYANG GENEX CORP.
XX PI Kim TJ, Park GH;
XX WPI; 2001-534477/59.
XX DR Manufacturing maltogenic amylase having improved transglycosylation
PT activity, comprises using crystallization.
XX PS Disclosure; Page 188; 196pp; Korean.
XX CC The present invention describes manufacturing maltogenic amylase (EC
CC 3.2.1.133) having improved transglycosylation activity, comprising using
CC crystallisation and the three dimensional structure of maltogenic

CC amylase. Manufacturing maltogenic amylase comprises the following steps:
CC (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC
CC 5027BP) and inserting the gene into plasmid pUC119 to construct
CC recombinant DNA (pThMAL19); (ii) inserting the recombinant DNA to
CC Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius
CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
CC supernatant through column chromatography and obtaining purified
CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two
CC maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase
CC (ThMA) crystal. The amylase has a structure containing an activated
CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
CC and a pocket with glucose bound that consists of amino acid residues of
CC Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn133, Glu132, Val132,
CC and His1360. The present sequence represents Aspergillus oryzae TAKA
CC protein (TAA), given in comparison with ThMA in the present invention
XX
SQ Sequence 423 AA;

Query Match 89.7%; Score 70; DB 4; Length 423;
Best Local Similarity 92.3%; Pred. No. 0.016;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
| | | | | | | | | |
Db 74 AMHGYWQDIYSL 86

RESULT 11
ABP97894
ID ABP97894 standard; protein; 494 AA.
XX AC ABP97894;
XX DT 17-JUN-2003 (first entry)
XX DE Amino acid sequence of an alpha-amylase of Aspergillus niger.
XX KW Alpha-amylase; enzyme; endohydrolysis; 1,4-alpha-glucosidic linkage;
XX KM oligosaccharide; polysaccharide; baking.
XX OS Aspergillus niger.
XX PN WO2003016535-A2.
XX PD 27-FEB-2003.
XX PF 02-AUG-2002; 2002WO-NL000522.
XX PR 16-AUG-2001; 2001EP-00000379.
XX PR 16-AUG-2001; 2001EP-00000380.
XX PR 16-AUG-2001; 2001EP-00000381.
XX PR 16-AUG-2001; 2001EP-00000382.
XX PR 16-AUG-2001; 2001EP-00000383.
XX PR 16-AUG-2001; 2001EP-00000384.
XX PA (STAM) DSM NV.
XX PI Maier D, Stock A, Wagner C, Folkers U, Albermann K, Hopper S;
XX WPI; 2003-312758/30.
XX DR New polynucleotide from a filamentous fungus, preferably Aspergillus
PT niger, useful in a baking process.
XX PS Claim 13; Page 61-63; 81pp; English.
XX CC The present sequence is an alpha-amylase enzyme of the filamentous fungus
CC Aspergillus niger. Alpha-amylases catalyse the endohydrolysis of 1,4-
CC alpha-glucosidic linkages in oligosaccharides and polysaccharides. The
CC alpha-amylase polynucleotides and polypeptides of the invention are
CC useful in a baking process

```

XX SQ Sequence 494 AA;
Query Match 89.7%; Score 70; DB 6; Length 494;
Best Local Similarity 84.6%; Pred. No. 0.019;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
DB 94 AYHGYWQDDIYSL 106

RESULT 12
AAR88213
ID AAR88213 standard; peptide; 55 AA.
XX
AC AAR88213;
XX
DT 16-OCT-2003 (revised)
DT 03-APR-1996 (first entry)
XX
DE Alpha-amylase fragment.
XX
KW Alpha-amylase; thermostable enzyme; baking; Thermomyces lanuginosus; PCR;
KW polymerase chain reaction.
XX
OS Thermomyces lanuginosus; CBS 223.63.
XX
PN WO9601323-A1.
XX
PD 18-JAN-1996.
XX
PF 03-JUL-1995; 95WO-EP002607.
XX
PR 04-JUL-1994; 94GB-00013419.
XX
PA (DANI-) DANISCO AS.
PI Michelsen B, Rasmussen P;
XX
DR WPI; 1996-087673/09.
XX
N-PSDB; AAT10565.
XX
PT Thermophilic alpha-amylase with activity range of 60-80 degrees C -
PT derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
PT and bakery prods. esp. bread.
XX
PS Disclosure; Page 40; 94pp; English.
XX
CC Fragments (AAR88213-14) of Thermomyces lanuginosus thermostable alpha-
CC amylase (AAR88212) are the products of DNA fragments (AAT10565-66)
CC generated from T. lanuginosus genomic DNA by PCR using primers based on
CC conserved regions of alpha-amylase genes. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 55 AA;
Query Match 88.5%; Score 69; DB 2; Length 55;
Best Local Similarity 76.9%; Pred. No. 0.0027;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
DB 26 SYHGYWQDDIYSL 38

RESULT 13
AAR88212
ID AAR88212 standard; protein; 493 AA.
XX
AC AAR88212;
XX
DT 16-OCT-2003 (revised)
XX

DT 03-APR-1996 (first entry)
XX
DE Alpha-amylase.
XX
KW Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
XX
OS Thermomyces lanuginosus; CBS 224.63.
XX
XX
XX Key Location/Qualifiers
XX FT 1. .18
XX FT Peptide
XX FT /label= Sig_peptide
XX
PN WO9601323-A1.
XX
PD 18-JAN-1996.
XX
PF 03-JUL-1995; 95WO-EP002607.
XX
PR 04-JUL-1994; 94GB-00013419.
XX
PA (DANI-) DANISCO AS.
PI Michelsen B, Rasmussen P;
XX
DR WPI; 1996-087673/09.
XX
N-PSDB; AAT10562.
XX
PT Thermophilic alpha-amylase with activity range of 60-80 degrees C -
PT derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
PT and bakery prods. esp. bread.
XX
PS Claim 3; Page 36-38; 94pp; English.
XX
CC A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS
CC 224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562)
CC isolated from a T. lanuginosus gene library. The recombinant enzyme (54-
CC 60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7
CC and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 493 AA;
Query Match 88.5%; Score 69; DB 2; Length 493;
Best Local Similarity 76.9%; Pred. No. 0.027;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
DB 98 SYHGYWQDDIYSL 110

RESULT 14
ADS23436
ID ADS23436 standard; protein; 500 AA.
XX
AC ADS23436;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #12469.
XX
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:40:32 ; Search time 0.810811 Seconds
(without alignments)
830.671 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 40

Sequence: 1 SSQDYFH 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	478	2 JK0201	alpha-amylase (EC 3.2.1.1)
2	40	100.0	498	2 A48305	alpha-amylase (EC 3.2.1.1)
3	40	100.0	499	1 ALAS1	alpha-amylase (EC 3.2.1.1)
4	40	100.0	499	1 ALAS3	alpha-amylase (EC 3.2.1.1)
5	40	100.0	499	2 JS0663	alpha-amylase (EC 3.2.1.1)
6	40	100.0	499	2 JT0466	alpha-amylase (EC 3.2.1.1)
7	40	100.0	499	2 JN0588	alpha-amylase (EC 3.2.1.1)
8	40	100.0	499	2 B48305	alpha-amylase (EC 3.2.1.1)
9	40	100.0	624	1 JC4510	pullulanase (EC 3.2.1.1)
10	34	85.0	130	2 H71415	hypothetical prote
11	33	82.5	420	2 T42616	envelope protein -
12	33	82.5	601	2 T18787	hypothetical prote
13	33	82.5	1131	2 T41943	major DNA binding
14	33	82.5	4351	2 T00252	MEGF1 protein - ra
15	32	80.0	144	2 JC7121	androgenic gland h
16	32	80.0	180	2 B95039	hypothetical prote
17	32	80.0	289	2 A43562	homeotic protein H
18	32	80.0	317	2 E84088	restriction endonu
19	32	80.0	351	2 E86187	YUP8H12.10 [impor
20	32	80.0	419	2 S61245	probable virion gl
21	32	80.0	419	2 T15199	hypothetical prote
22	32	80.0	482	2 A90248	conserved hypothet
23	32	80.0	685	2 S67146	probable membrane
24	32	80.0	820	1 DEECK	thra bifunctional
25	32	80.0	820	2 B85480	aspartokinase I, h
26	32	80.0	820	2 B90629	aspartokinase I, h
27	32	80.0	820	2 AC0502	aspartokinase I/ho
28	31	77.5	67	2 T17658	hypothetical prote
29	31	77.5	104	2 S49803	hypothetical prote

30	31	77.5	214	2 B75513	pyridoxamine 5-pho
31	31	77.5	261	2 AF1307	hypothetical prote
32	31	77.5	261	2 AF1679	hypothetical prote
33	31	77.5	386	2 S72435	RNA-binding protei
34	31	77.5	461	2 F86597	UDP-glucose pyroph
35	31	77.5	461	2 H72024	UDP-N-acetylglucos
36	31	77.5	597	2 T35746	hypothetical prote
37	31	77.5	614	1 I48385	RNA helicase TN22
38	31	77.5	614	2 JC1087	RNA helicase, ATP-
39	31	77.5	668	2 T10575	hypothetical prote
40	31	77.5	825	2 S55060	feritin alpha-II
41	31	77.5	893	2 T03864	hypothetical prote
42	31	77.5	905	2 S55059	feritin alpha-I -
43	30	75.0	182	2 AE2146	hypothetical prote
44	30	75.0	194	2 T22209	hypothetical prote
45	30	75.0	229	2 A89473	protein F52D2.2 [i

ALIGNMENTS

RESULT 1

JK0201

alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae

N:Alternate names: glycogenase; Taka-amylase A

C:Species: Aspergillus oryzae

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C:Accession: JK0201

R: Toda, H.; Kondo, K.; Narita, K.

Proc. Jpn. Acad. 58B, 208-212, 1982

A: Title: The complete amino acid sequence of Taka-amylase A.

A: Reference number: JK0201

A: Accession: JK0201

A: Molecule type: protein

A: Residues: 1-478 <TOD>

A: Cross-references: UNIPROT: P10529

C: Comment: One atom of calcium per molecule is essential for the activity.

C: Comment: This enzyme is a glycoprotein.

C: Comment: See also PIR:JT0466 and PIR:JS0240.

C: Function:

A: Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A: Pathway: glycogen/starch degradation

C: Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C: Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F: 173-300/Domain: alpha-amylase core homology <AMY>

F: 197/Binding site: carbohydrate (Asn) (covalent) #status experimental

F: 210,230,297/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 40; DB 2; Length 478;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

Db 141 SSQDYFH 147

RESULT 2

A48305

alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori

C: Species: Aspergillus awamori

C: Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C: Accession: A48305

R: Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;

Curr. Genet. 17, 203-212, 1990

A: Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe

A: Reference number: A48305; MUID: 90254827; PMID: 2340591

A: Accession: A48305

A: Status: preliminary; not compared with conceptual translation

A: Molecule type: DNA

A: Residues: 1-498 <KOR>

A: Cross-references: UNIPROT: Q02905

C: Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
 C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
 F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 40; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 1.5; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||

Db 162 SSQDYFH 168

RESULT 3

ALAS1

Alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
 N;Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
 C;Species: Aspergillus oryzae
 C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
 C;Accession: S04548; A33214; J50240; A91930; A93767; A10627
 R;Wirsel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.
 Mol. Microbiol. 3, 3-14, 1989

A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
 A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Accession: S04548

A;Molecule type: DNA

A;Residues: 1-499 <WIR>

A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921

A;Genetics: AMY1

A;Accession: A33214

A;Molecule type: mRNA

A;Residues: 1-499 <WID>

A;Cross-references: GB:X12725; NID:g2430; PIDN:CAA31218.1; PID:g295921

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989

A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing

A;Reference number: J50240; MUID:89378767; PMID:2789162

A;Accession: J50240

A;Molecule type: DNA

A;Residues: 1-499 <GEN>

A;Genetics: AMY2

A;Note: the authors refer to this as isozyme II

R;Isemura, S.; Ikenaka, T.

J. Biochem. 74, 1-10, 1973

A;Reference number: A91930; MUID:74001521; PMID:4733850

A;Accession: A91930

A;Molecule type: protein

A;Residues: 206-225 <ISE>

R;Narita, K.

Proc. Jpn. Acad. 51, 285-290, 1975

A;Reference number: A93767

A;Accession: A93767

A;Molecule type: protein

A;Residues: 434-443, 446-447, 'Q', 449-458, 'GTTV', 459-464, 467-468, 'B', 470, 'B', 472-499 <NAR>

R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A;Title: Structure and possible catalytic residues of Taka-amylase A.

A;Reference number: A37454; MUID:84212370; PMID:6609921

A;Contents: annotation; X-ray crystallography, 3.0 angstroms

R;Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkmenburg, J.P.; Wilkinson, A.

submitted to the Brookhaven Protein Data Bank, August 1992

A;Reference number: A51548; PDB:6TAA

A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497

C;Comment: One atom of calcium per molecule is essential for activity.

C;Genetics: <AMY1>

A;Gene: amy1

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Genetics: <AMY2>

A;Gene: amy2; AmyII

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
 C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-499/Product: alpha-amylase 1 #status experimental <MAT>
 F;194-321/Domain: alpha-amylase core homology <AMY>
 F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
 F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
 F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 40; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 1.5; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||

Db 162 SSQDYFH 168

RESULT 4

ALAS3

Alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae

N;Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A

C;Species: Aspergillus oryzae

C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004

C;Accession: S04549; A33215; A44713

R;Wirsel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon

A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Accession: S04549

A;Molecule type: DNA

A;Residues: 1-499 <WIR>

A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922

A;Accession: A33215

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-499 <WID>

A;Cross-references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989

A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing

A;Reference number: J50240; MUID:89378767; PMID:2789162

A;Accession: A44713

A;Molecule type: DNA

A;Residues: 1-499 <GEN>

A;Note: the authors refer to this as isozyme I

R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A;Title: Structure and possible catalytic residues of Taka-amylase A.

A;Reference number: A37454; MUID:84212370; PMID:6609921

A;Contents: annotation; X-ray crystallography, 3.0 angstroms

C;Comment: One atom of calcium per molecule is essential for activity.

C;Genetics:

A;Gene: amy3; AmyI

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; metal

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-499/Product: alpha-amylase 3 #status experimental <AMY>

F;194-321/Domain: alpha-amylase core homology <AMY>

F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental

F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted

F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 40; DB 1; Length 499;

Best Local Similarity 100.0%; Pred. No. 1.5;


```
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 5
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
NAlternate names: Aspergillus sp.
CSpecies: Aspergillus sp.
CDate: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
CAccession: J00663
R;Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A>Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyamii and its expression
A|Reference number: J00663; MUID:92323146; PMID:1368777
A|Accession: J00663
A|Molecule type: mRNA
A|Residues: 1-499 <SHI>
C|Function:
A|Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A|Pathway: glycogen/starch degradation
C|Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C|Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F|1-21/DNA: signal sequence #status predicted <SIG>
F|22-499/Product: alpha-amylase #status predicted <ALP>
F|194-321/DNA: alpha-amylase core homology <AMY>
F|218/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 6
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
NAlternate names: glycogenase, Taka-amylase A
CSpecies: Aspergillus oryzae
CDate: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
CAccession: J00466
R;Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A>Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus
A|Reference number: J00466
A|Accession: J00466
A|Molecule type: DNA
A|Residues: 1-499 <TAD>
A|Cross-references: UNIPROT:P10529
C|Comment: See also PIR:JK0201 and PIR:JS0240.
C|Comment: One atom of calcium per molecule is essential for activity.
C|Genetics:
A|Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C|Function:
A|Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A|Pathway: glycogen/starch degradation
C|Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C|Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F|1-21/DNA: signal sequence #status predicted <SIG>
F|22-499/Product: alpha-amylase #status predicted <MAT>
F|194-321/DNA: alpha-amylase core homology <AMY>
F|218/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 7
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
NAlternate names: Taka-amylase A
CSpecies: Aspergillus oryzae
CDate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
CAccession: JN0588
R;Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kiritani, N.; Tsuboi, A.; Uda, S.
Gene 84, 319-327, 1989
A>Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m
A|Reference number: JN0588; MUID:90128276; PMID:2612911
A|Accession: JN0588
A|Molecule type: mRNA
A|Residues: 1-499 <TSU>
A|Cross-references: UNIPROT:Q96TH4
C|Comment: The alpha amylases are encoded by multigene family.
C|Genetics:
A|Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C|Function:
A|Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A|Pathway: glycogen/starch degradation
C|Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C|Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F|1-21/DNA: signal sequence #status predicted <SIG>
F|22-499/Product: alpha-amylase #status predicted <MAT>
F|194-321/DNA: alpha-amylase core homology <AMY>
F|218/Binding site: carboxylate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 8
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
CSpecies: Aspergillus awamori
CDate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
CAccession: B48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A>Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe
A|Reference number: B48305; MUID:90254827; PMID:2340591
A|Accession: B48305
A|Status: preliminary; not compared with conceptual translation
A|Molecule type: DNA
A|Residues: 1-499 <KOR>
A|Cross-references: UNIPROT:Q02906
C|Function:
A|Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A|Pathway: glycogen/starch degradation
C|Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C|Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F|194-321/DNA: alpha-amylase core homology <AMY>
Query Match 100.0%; Score 40; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168
```

RESULT 9
JC4510
pullulanase (EC 3.2.1.41) precursor - yeast (*Lipomyces kononenkoae*)
N:Alternate names: LKA1 protein; raw starch-degrading amylase
N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C:Species: *Lipomyces kononenkoae*
C:Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4510; PC4116
R:Steyn, A.J.-C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a LipD
A:Reference number: JC4510; MUID:96105202; PMID:8529895
A:Accession: JC4510
A:Molecule type: mRNA
A:Residues: 1-624 <STE>
A:Cross-references: UNIPROT:Q01117; GB:U03076; NID:g1173536; PIDN:AAC49622.1; PID:g11735
A:Experimental source: strain IGC4052B
A:Accession: PC4116
A:Molecule type: protein
A:Residues: 29-44 <ST2>
A:Experimental source: IGC4052B
C:Genetics:
A:Gene: LKA1
C:Function:
A:Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
A:Pathway: glycogen/starch degradation
C:Superfamily: lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-624/Product: alpha-amylase #status predicted <MAT>
F:48-141/Domain: glucoamylase starch-binding domain homology <SBD>
F:320-447/Domain: alpha-amylase core homology <AMY>
F:177-185,297-311,387-430,587-622/Disulfide bonds: #status predicted
F:304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 40; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

QY 1 SSQDYFH 7
DB 288 SSQDYFH 294

RESULT 10
H71415
hypothetical protein - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cross)
A:Variety: Columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: H71415
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thal*
A:Reference number: A71400; MUID:98121113; PMID:9461215
A:Accession: H71415
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-130 <BEV>
A:Cross-references: UNIPROT:O23373; GB:Z97338; NID:g2244870; PID:e326912; PID:g2244877
C:Genetics:
A:Map position: 4COP9-4G3845

Query Match 85.0%; Score 34; DB 2; Length 130;
Best Local Similarity 85.7%; Pred. No. 6.1; Mismatches 0; Indels 1; Gaps 0;
Matches 6; Conservative 0

QY 1 SSQDYFH 7
DB 38 SSADYFH 44

RESULT 11
T42616
envelope protein - equine herpesvirus 4 (strain NS80567)
C:Species: equine herpesvirus 4
A:Variety: strain NS80567
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42616
R:Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998
A:Title: The DNA sequence of equine herpesvirus-4.
A:Reference number: Z22173; MUID:98264497; PMID:9603335
A:Accession: T42616
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-420 <TEL>
A:Cross-references: UNIPROT:O39309; EMBL:AF030027; NID:g2605950; PIDN:AAC59593.1; PID:g2
A:Experimental source: strain NS80567
C:Genetics:
A:Note: 73
C:Superfamily: pseudorabies virus glycoprotein gp63

Query Match 82.5%; Score 33; DB 2; Length 420;
Best Local Similarity 83.3%; Pred. No. 36; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1

QY 2 SODYFH 7
DB 114 NODYFH 119

RESULT 12
T18787
hypothetical protein BE10.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18787
R:McMurray, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19022
A:Accession: T18787
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-601 <WIL>
A:Cross-references: UNIPROT:O17552; EMBL:Z93372; PIDN:CAB07545.1; GSPDB:GN00021; CBSP:BE1
C:Experimental source: clone BE10
C:Genetics:
A:Gene: CESP:BE10.3
A:Map position: 3
A:Introns: 21/3; 54/3; 117/2; 157/1; 212/2; 533/3

Query Match 82.5%; Score 33; DB 2; Length 601;
Best Local Similarity 71.4%; Pred. No. 53; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 2

QY 1 SSQDYFH 7
DB 453 NSQDYFH 459

RESULT 13
T41943
major DNA binding protein - human herpesvirus 7 (strain JI)
C:Species: human herpesvirus 7
A:Variety: strain JI
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41943
R:Nicholas, J.

submitted to the EMBL Data Library, December 1995

A;Description: Determination and analysis of the complete nucleotide sequence of human h
A;Reference number: Z22022
A;Accession: T41943
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1131 <NIC>
A;Cross-references: UNIPROT:P52339; EMBL:U43400; PIDN:AAC54703.1
A;Experimental source: strain JI
C;Genetics:
A;Note: U41
C;Superfamily: herpesvirus DNA-binding protein

Query Match 82.5%; Score 33; DB 2; Length 1131;

Best Local Similarity 71.4%; Pred. No. 1.1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

DB 943 ASRDYFH 949

RESULT 14

T00252

MEGF1 protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C;Accession: T00252

R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998

A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A;Reference number: Z14126; MUID:98360089; PMID:9693030

A;Accession: T00252

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-4351 <NAK>

A;Cross-references: UNIPROT:O88277; EMBL:AB011527; NID:G3449285; PIDN:BAA32458.1; PID:93

A;Experimental source: brain

C;Genetics:

A;Gene: MEGF1

C;Superfamily: rat MEGF1 protein; cadherin repeat homology; EGF homology; laminin G repe

F;3798-3949/Domain: laminin G repeat homology <LGR>

F;3953-3985/Domain: EGF homology <EGF>

F;3992-4023/Domain: EGF homology <EGF1>

Query Match 82.5%; Score 33; DB 2; Length 4351;

Best Local Similarity 71.4%; Pred. No. 4.6e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

DB 605 NEQDYFH 611

RESULT 15

JC7121

androgenic gland hormone precursor - common pill bug

C;Species: Armadillidium vulgare (common pill bug)

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C;Accession: JC7121

R;Okuno, A.; Hasegawa, Y.; Ohira, T.; Katakura, Y.; Nagasawa, H.

Biochem. Biophys. Res. Commun. 264, 419-423, 1999

A;Title: Characterization and cDNA cloning of androgenic gland hormone of the terrestria

A;Reference number: JC7121; MUID:20001935; PMID:10529379

A;Accession: JC7121

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-144 <OKU>

A;Cross-references: UNIPROT:Q9UR82; DBJ:AB029615; GB:AB029615; NID:G6446571; PID:G64465

A;Experimental source: androgenic gland

Query Match 80.0%; Score 32; DB 2; Length 144;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7

DB 82 QDYFH 86

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Job time : 1.81081 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:04 ; Search time 6.95174 Seconds.
(without alignments)
782.441 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110

Perfect score: 13

Sequence: 1 AYHGYWQDDIYSL 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1867879 seqs, 418409474 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	476	17	US-10-877-849-43
2	13	100.0	478	14	US-10-184-771-10
3	13	100.0	478	14	US-10-186-042-7
4	13	100.0	478	15	US-10-644-187-7
5	13	100.0	478	17	US-10-926-720-10
6	13	100.0	478	17	US-10-980-759-7
7	13	100.0	478	20	US-11-064-196-10
8	13	100.0	498	16	US-10-815-495-22
9	13	100.0	498	16	US-10-820-200-2
10	13	100.0	498	17	US-10-877-849-30
11	13	100.0	499	16	US-10-815-495-18

12	13	100.0	499	16	US-10-797-393A-5	Sequence 5, Appli
13	13	100.0	608	17	US-10-877-849-40	Sequence 40, Appl
14	13	100.0	640	17	US-10-877-849-36	Sequence 36, Appl
15	13	100.0	1095	14	US-10-228-063-45	Sequence 45, Appl
16	12	92.3	495	14	US-10-213-990-42	Sequence 42, Appl
17	9	69.2	494	17	US-10-486-868-13	Sequence 13, Appl
18	8	61.5	484	15	US-10-416-393-1	Sequence 1, Appli
19	8	61.5	484	16	US-10-797-393A-1	Sequence 1, Appli
20	8	61.5	505	17	US-10-877-849-42	Sequence 42, Appl
21	8	61.5	511	17	US-10-877-849-8	Sequence 8, Appli
22	8	61.5	609	17	US-10-877-849-38	Sequence 38, Appl
23	8	61.5	629	17	US-10-877-849-34	Sequence 34, Appl
24	8	61.5	640	17	US-10-877-007-22	Sequence 22, Appl
25	8	61.5	640	17	US-10-877-849-32	Sequence 32, Appl
26	8	61.5	640	17	US-10-877-849-41	Sequence 41, Appl
27	7	53.8	630	14	US-10-213-990-45	Sequence 45, Appl
28	6	46.2	175	15	US-10-424-599-258851	Sequence 258851,
29	6	46.2	190	16	US-10-425-115-279730	Sequence 279730,
30	6	46.2	252	16	US-10-425-115-239140	Sequence 239140,
31	6	46.2	429	15	US-10-369-493-22639	Sequence 22639, A
32	6	46.2	483	15	US-10-369-493-597	Sequence 597, App
33	6	46.2	493	15	US-10-369-493-22723	Sequence 22723, A
34	6	46.2	500	15	US-10-369-493-12469	Sequence 12469, A
35	6	46.2	513	15	US-10-369-493-2223	Sequence 2223, Ap
36	6	46.2	547	14	US-10-213-990-48	Sequence 48, Appl
37	6	46.2	549	17	US-10-486-868-14	Sequence 14, Appl
38	6	46.2	555	17	US-10-486-868-15	Sequence 15, Appl
39	6	46.2	564	15	US-10-369-493-22679	Sequence 22679, A
40	6	46.2	567	17	US-10-486-868-18	Sequence 18, Appl
41	6	46.2	583	17	US-10-732-923-7439	Sequence 7439, Ap
42	6	46.2	647	17	US-10-732-923-7480	Sequence 7480, Ap
43	6	46.2	686	17	US-10-872-198-44	Sequence 44, Appl
44	6	46.2	686	17	US-10-872-197A-44	Sequence 44, Appl
45	6	46.2	686	18	US-10-787-219A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-10-877-849-43
; Sequence 43, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

Query Match 100.0%; Score 13; DB 17; Length 476;

Best Local Similarity 100.0%; Pred. No. 1.1e-06; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13

Db 78 AYHGYWQDDIYSL 90

RESULT 2
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1f216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match 100.0%; Score 13; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQQDIYSL 13
Db 78 AYHGYYQQDIYSL 90
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RESULT 3
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 100.0%; Score 13; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQQDIYSL 13
Db 78 AYHGYYQQDIYSL 90
|||||

RESULT 4
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match 100.0%; Score 13; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQQDIYSL 13
Db 78 AYHGYYQQDIYSL 90
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RESULT 5
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475

REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 100.0%; Score 13; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
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Db 78 AYHGYWQDDIYSL 90

RESULT 6

US-10-980-759-7
; Sequence 7, Application US/10980759
; Publication No. US20050118695A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/980,759
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-980-759-7

Query Match 100.0%; Score 13; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
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Db 78 AYHGYWQDDIYSL 90

RESULT 7

US-11-064-196-10
; Sequence 10, Application US/11064196
; Publication No. US20050170487A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/11/064,196
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-11-064-196-10

Query Match 100.0%; Score 13; DB 20; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
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Db 78 AYHGYWQDDIYSL 90

RESULT 8

US-10-815-495-22
; Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connolly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 100.0%; Score 13; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
Db 99 AYHGYWQDDIYSL 111

RESULT 9

US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Pedersen, Sven
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2

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; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match      100.0%; Score 13; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
DB 98 AYHGYWQDDIYSL 110
|||||

RESULT 10
US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match      100.0%; Score 13; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
DB 98 AYHGYWQDDIYSL 110
|||||

RESULT 11
US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connolly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match      100.0%; Score 13; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
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DB 99 AYHGYWQDDIYSL 111

RESULT 12
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Feestersen, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match      100.0%; Score 13; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
DB 99 AYHGYWQDDIYSL 111
|||||

RESULT 13
US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

Query Match      100.0%; Score 13; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
|||||
DB 98 AYHGYWQDDIYSL 110
|||||

RESULT 14
US-10-877-849-36
; Sequence 36, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
```


; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 13; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||
Db 98 AYHGYWQDIYSL 110

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lananan, Mike
; TITLE OF INVENTION: Self-processing plants and plant parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 100.0%; Score 13; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||
Db 78 AYHGYWQDIYSL 90

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Job time : 7.95174 secs

Large work group

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2005, 18:45:18 ; Search time 1.95753 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AVHGWQDIYSL 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

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- 6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	478	1 US-08-720-899-7	Sequence 7, Appli
2	13	100.0	478	1 US-08-459-610-7	Sequence 7, Appli
3	13	100.0	478	2 US-08-343-804-7	Sequence 7, Appli
4	13	100.0	478	2 US-08-600-908A-10	Sequence 10, Appl
5	13	100.0	478	3 US-08-683-838A-10	Sequence 10, Appl
6	13	100.0	478	3 US-09-182-859-7	Sequence 7, Appli
7	13	100.0	478	4 US-09-672-459-7	Sequence 7, Appli
8	13	100.0	478	4 US-09-636-252A-10	Sequence 10, Appl
9	13	100.0	478	4 US-10-186-042-7	Sequence 7, Appli
10	6	46.2	14	1 US-08-204-656B-11	Sequence 11, Appl
11	6	46.2	14	1 US-08-204-656B-12	Sequence 12, Appl
12	6	46.2	14	1 US-08-470-702-11	Sequence 11, Appl
13	6	46.2	14	1 US-08-470-702-12	Sequence 12, Appl
14	6	46.2	14	1 US-08-467-831-11	Sequence 11, Appl
15	6	46.2	14	1 US-08-467-831-12	Sequence 12, Appl
16	6	46.2	31	1 US-08-190-802A-234	Sequence 234, App
17	6	46.2	31	3 US-08-477-346-234	Sequence 234, App
18	6	46.2	31	3 US-08-473-089-234	Sequence 234, App
19	6	46.2	31	4 US-08-487-072A-234	Sequence 234, App
20	6	46.2	394	4 US-09-248-796A-18703	Sequence 18703, A
21	6	46.2	514	4 US-09-108-857-2	Sequence 2, Appli
22	6	46.2	685	3 US-08-947-965-72	Sequence 72, Appl
23	6	46.2	685	3 US-08-947-965-74	Sequence 74, Appl
24	6	46.2	686	3 US-08-947-965-70	Sequence 70, Appl
25	6	46.2	686	3 US-08-947-965-73	Sequence 73, Appl
26	6	46.2	713	1 US-08-190-802A-63	Sequence 63, Appl
27	6	46.2	713	3 US-08-477-346-63	Sequence 63, Appl

28	6	46.2	713	3 US-08-473-089-63	Sequence 63, Appl
29	6	46.2	713	4 US-08-487-072A-63	Sequence 63, Appl
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31	6	46.2	833	3 US-09-514-302-3	Sequence 3, Appli
32	6	46.2	833	4 US-10-014-436-3	Sequence 3, Appli
33	6	46.2	1938	3 US-09-514-302-2	Sequence 2, Appli
34	6	46.2	1938	4 US-10-014-436-2	Sequence 2, Appli
35	5	38.5	8	4 US-09-108-857-7	Sequence 7, Appli
36	5	38.5	13	2 US-08-870-864-2	Sequence 2, Appli
37	5	38.5	30	4 US-09-471-276-1105	Sequence 1105, Ap
38	5	38.5	61	3 US-08-858-207A-538	Sequence 538, App
39	5	38.5	87	4 US-09-583-110-3205	Sequence 3205, Ap
40	5	38.5	90	4 US-09-107-433-4734	Sequence 4734, Ap
41	5	38.5	129	4 US-10-101-464A-609	Sequence 609, App
42	5	38.5	131	4 US-09-270-767-32792	Sequence 32792, A
43	5	38.5	131	4 US-09-270-767-48009	Sequence 48009, A
44	5	38.5	133	4 US-10-101-464A-485	Sequence 485, App
45	5	38.5	136	4 US-09-270-767-32469	Sequence 32469, A

ALIGNMENTS

RESULT 1

US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-720-899-7

Query Match 100.0%; Score 13; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 2
US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match 100.0%; Score 13; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 580837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 580837o No. 580837disk of No. 580837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match 100.0%; Score 13; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 4
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-343-804-7

Query Match 100.0%; Score 13; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 5
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-343-804-7
```

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-600-908A-10

Query Match          100.0%; Score 13; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 5
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Prantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6022724dsk of No. 6022724dsk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-683-838A-10

Query Match          100.0%; Score 13; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 6
US-09-182-859-7
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; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Prantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7

Query Match          100.0%; Score 13; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90

RESULT 7
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Prantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match          100.0%; Score 13; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
Db      78 AYHGYWQDDIYSL 90
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RESULT 8
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1f218-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
; PRIORITY FILING DATE: 2000-08-10
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10

Query Match      100.0%; Score 13; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
DB      78 AYHGYWQDDIYSL 90

RESULT 9
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; PRIORITY FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1995-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match      100.0%; Score 13; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYWQDDIYSL 13
DB      78 AYHGYWQDDIYSL 90
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RESULT 10
US-08-204-656B-11
; Sequence 11, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuro
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase.
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-204-656B-11

Query Match      46.2%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYHGYW 6
DB      7 AYHGYW 12

RESULT 11
US-08-204-656B-12
; Sequence 12, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuro
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
```

STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiner, Marc S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-204-656B-12

Query Match 46.2%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 7 AYHGYW 12

RESULT 12
US-08-470-702-11
Sequence 11, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION INFORMATION:

APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-470-702-11

Query Match 46.2%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 7 AYHGYW 12

RESULT 13
US-08-470-702-12
Sequence 12, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION INFORMATION:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:25:16 ; Search time 291.301 Seconds
(without alignments)
661.194 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 2684
Sequence: 1 NVAWSLFLYGLQVAPALA.....LPRVLYPTKLAGSKICSSS 498

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A: Geneseq 16Dec04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2684	100.0	498	AAB84206	AAB84206 Amino aci
2	2674	99.6	499	ADT89628	ADT89628 Aspergill
3	2662	99.2	498	ADT89632	ADT89632 Aspergill
4	2572	95.8	478	AAR72450	AAR72450 Aspergill
5	2572	95.8	478	AAR78270	AAR78270 Aspergill
6	2572	95.8	478	AAR14500	AAR14500 Aspergill
7	2569	95.7	1095	ABP96630	ABP96630 Alpha-amyl
8	2552	95.1	478	AAR46065	AAR46065 Mutant al
9	2503.5	93.3	478	AAR79025	AAR79025 Mature ta
10	2151	80.1	423	ABB09072	ABB09072 Aspergill
11	2100	78.2	495	ABB80177	ABB80177 A. fumiga
12	2012	75.0	494	ABP97894	ABP97894 Amino aci
13	1835	68.4	630	ABB80178	ABB80178 A. fumiga
14	1778	66.2	484	AAE24207	AAE24207 Aspergill
15	1778	66.2	484	ADS75939	ADS75939 Aspergill
16	1666.5	62.1	493	AAR88212	AAR88212 Alpha-amyl
17	1449	54.0	512	AAR07574	AAR07574 Alpha-amyl
18	1400.5	52.2	511	AAP81180	AAP81180 Sequence
19	1398.5	52.1	511	AAR81161	AAR81161 Recombina
20	1397	52.0	468	AAR24136	AAR24136 Alpha-amyl
21	1396.5	52.0	494	AAP70571	AAP70571 Alpha-amyl
22	1392	51.9	468	AAR63184	AAR63184 Variant a
23	1391	51.8	468	AAR63185	AAR63185 Variant a
24	1387	51.7	468	AAR63187	AAR63187 Variant a
25	1338	49.9	452	AAR63186	AAR63186 Variant a

26	1214.5	45.2	547	6	ABB80179	ABB80179 A. fumiga
27	1183	44.1	555	6	ABP97896	ABP97896 Amino aci
28	1163	43.3	567	6	ABP97899	ABP97899 Amino aci
29	1160	43.2	500	8	ADS23436	ADS23436 Bacterial
30	1085	40.4	549	6	ABP97895	ABP97895 Amino aci
31	1015.5	37.8	513	8	ADN19570	ADN19570 Bacterial
32	898.5	33.5	564	8	ADS44249	ADS44249 Bacterial
33	873	32.5	493	8	ADS44293	ADS44293 Bacterial
34	541	20.2	502	6	ABU03092	ABU03092 Alpha amy
35	483.5	18.0	547	8	ADS30907	ADS30907 Bacterial
36	480.5	17.9	547	8	ADS30029	ADS30029 Bacterial
37	456.5	17.0	713	7	ADC23483	ADC23483 Bacillus
38	453	16.9	719	4	AAB74220	AAB74220 Bacillus
39	452.5	16.9	712	2	AAR10051	AAR10051 Cyclomalt
40	452	16.8	719	4	AAB74219	AAB74219 Bacillus
41	450	16.8	719	2	AAY31731	AAY31731 Bacillus
42	450	16.8	719	2	AAY30621	AAY30621 Amino aci
43	450	16.8	719	3	AAY94271	AAY94271 Bacillus
44	450	16.8	719	4	AAB59956	AAB59956 Bacillus
45	450	16.8	719	4	AAB74216	AAB74216 Bacillus

ALIGNMENTS

RESULT 1
AAB84206
ID AAB84206 standard; protein; 498 AA.
XX AC AAB84206;
XX DT 06-AUG-2001 (first entry)
XX DE Amino acid sequence of a fungamyl-like alpha-amylase.
XX KW Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
XX KW alcohol; starch; dough improver; brewing; starch liquification.
XX OS Aspergillus oryzae.
XX PN WO200134784-A1.
XX PD 17-MAY-2001.
XX PF 10-NOV-2000; 2000WO-DK000626.
XX PR 10-NOV-1999; 99DK-00001617.
XX PA (NOVO) - NOVOZYMES AS.
XX PI Bisgard-Frantzen H, Svendsen A, Pedersen S;
XX DR WPI; 2001-367478/38.
XX DR N-PSDB; AAF90208.
XX PT New variant of Fungamyl-like alpha-amylase, useful for production of
PT maltose syrups, includes mutations that improve stability against heat
PT and acidic pH.
XX PS Claim 1; Page 42-45; 49pp; English.
XX CC The present sequence represents a fungamyl-like alpha-amylase. The
CC specification describes variants of this fungamyl-like alpha-amylase,
CC which have an alteration in one the amino acid regions 98-110, 150-160,
CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
CC substitution of an amino acid or an insertion of an amino acid downstream
CC of a particular position. The variants retain alpha-amylase activity, and
CC have better heat stability and/or stability at acidic pH, relative to
CC wild-type enzyme. The variants can therefore be used at higher
CC temperatures (more efficient conversion or faster reaction, and have
CC reduced need for cooling and reduced risk of contamination). The variants
CC may also be used in conjunction with other enzymes, particularly
CC glucoamylase during dextrinisation. The variants are used to produce

CC syrups, particularly of high maltose content, or alcohol, from starch; as
CC dough improver for baked goods; in brewing, to increase fermentability of
CC the wort; and for liquefaction of starch

XX Sequence 498 AA;

Query Match 100.0%; Score 2684; DB 4; Length 498;
Best Local Similarity 100.0%; Pred. No. 3e-226;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGG 60
DB 1 MVAWWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGG 60
QY 61 TWQGIIDKLDYIQGMGFTAIWITPTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 120
DB 61 TWQGIIDKLDYIQGMGFTAIWITPTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 120
QY 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGLSVNSYIDGLRIDTVKHVKQDFWPVGN 240
DB 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGLSVNSYIDGLRIDTVKHVKQDFWPVGN 240
QY 241 KAAGYVCIGEVLGDGPATYCPYQNVMDGVNLNPIYYPILLNAPKSTSGSMDDLYNNINTVK 300
DB 241 KAAGYVCIGEVLGDGPATYCPYQNVMDGVNLNPIYYPILLNAPKSTSGSMDDLYNNINTVK 300
QY 301 SDPCDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAIILNDGPIIYAGQEHYAGGND 360
DB 301 SDPCDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAIILNDGPIIYAGQEHYAGGND 360
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRGT 420
DB 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRGT 420
QY 421 DGSQIVTILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
DB 421 DGSQIVTILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
QY 481 RVLYPEKLAGSKICSSS 498
DB 481 RVLYPEKLAGSKICSSS 498

RESULT 2
ADT89628
ID ADT89628 standard; protein; 499 AA.
XX AC ADT89628;
XX

DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase B (amyB) protein.
XX
KW Glucoamylase; glaa; amyB; alpha-amylase B; enzyme.
XX
OS Aspergillus niger.

XX US2004191864-A1.
XX 30-SEP-2004.
XX
XX 31-MAR-2004; 2004US-00815495.
XX
XX 31-MAR-2003; 2003US-0459902P.
XX
XX (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX

DR WPI: 2004-708545/69.
DR N-PSDB; ADT89627.

XX Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.

PS Example 10; SEQ ID NO 19; 59pp; English.

XX The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase B (amyB) protein.

XX Sequence 499 AA;

Query Match 99.6%; Score 2674; DB 8; Length 499;
Best Local Similarity 99.6%; Pred. No. 2.3e-225;
Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAWWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGG 60
DB 2 MVAWWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRPARTDGGTTATCNTADQKCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 121
QY 121 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGLSVNSYIDGLRIDTVKHVKQDFWPVGN 240
DB 182 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGLSVNSYIDGLRIDTVKHVKQDFWPVGN 241
QY 241 KAAGYVCIGEVLGDGPATYCPYQNVMDGVNLNPIYYPILLNAPKSTSGSMDDLYNNINTVK 300
DB 242 KAAGYVCIGEVLGDGPATYCPYQNVMDGVNLNPIYYPILLNAPKSTSGSMDDLYNNINTVK 301
QY 301 SDPCDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAIILNDGPIIYAGQEHYAGGND 360
DB 302 SDPCDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAIILNDGPIIYAGQEHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRGT 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRGT 421
QY 421 DGSQIVTILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 481
QY 481 RVLYPEKLAGSKICSSS 498
DB 482 RVLYPEKLAGSKICSSS 499

RESULT 3
ADT89632
ID ADT89632 standard; protein; 498 AA.
XX AC ADT89632;
XX
DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
KW Glucoamylase; glaa; amyA; alpha-amylase A; enzyme.

XX OS Aspergillus niger.
XX PN US2004191864-A1.
XX PD 30-SEP-2004.
XX PF 31-MAR-2004; 2004US-00815495.
XX PR 31-MAR-2003; 2003US-0459902P.
XX PA (NOVO) NOVOZYMES BIOTECH INC.
XX PI Connelly M, Brody H;
XX WPI; 2004-708545/69.
DR N-PSDB; ADT89631.
XX Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX Example 11; SEQ ID NO 22; 58pp; English.
XX The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glax) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX Sequence 498 AA;
SQ

Query Match 99.2%; Score 2662; DB 8; Length 498;
Best Local Similarity 99.6%; Pred. No. 2.6e-224;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLTLDRFARTDGGTTATCNTADOKYCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLTLDRFARTDGGTTATCNTADOKYCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDAYHGYWQDIYSLNENYGTADDL 121
QY 121 KALSSALHERGMYLVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTQ 180
DB 122 KALSSALHERGMYLVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTQ 181
QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYN 240
DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYN 241
QY 241 KAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNPIYYPLLNAPKSTSGSMDDLNNMINTVK 300
DB 242 KAAGVYICIGEVLDGDPAYTCPYQNVMDGVLNPIYYPLLNAPKSTSGSMDDLNNMINTVK 301
QY 301 SDCPSTLLGTFFVENHNDPRFASYTNDIALAKNVAFAIILNDGIPIIYAGQSQHYAGGND 360
DB 302 SDCPSTLLGTFFVENHNDPRFASYTNDIALAKNVAFAIILNDGIPIIYAGQSQHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLASANAIRNYAISKDTGFTVTKNPIYKDDTTIARKGT 420
DB 362 PANREATWLSGYPTDSELYKLASANAIRNYAISKDTGFTVTKNPIYKDDTTIARKGT 421
QY 421 DGSQIVTILSNKASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTSGDGNVFPVMAGGLP 480
DB 422 DGSQIVTILSNKASGDSYTLISLGSAGYTAGQQLTEVIGCTTIVTSGDGNVFPVMAGGLP 481
QY 481 RVLYPTEKLAGSKIC 495

DB 482 RVLYPTEKLAGSKIC 496
|||||
RESULT 4
AAR72450
ID AAR72450 standard; protein; 478 AA.
XX AC AAR72450;
XX DT 25-MAR-2003 (revised)
XX DT 01-DEC-1995 (first entry)
XX DE Aspergillus oryzae alpha amylase (mature protein).
XX KW Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
KW thermostable.
XX OS Aspergillus oryzae.
XX PN WO9510603-A1.
XX PD 20-APR-1995.
XX PF 05-OCT-1994; 94WO-DK000370.
XX PR 08-OCT-1993; 93DK-00001133.
XX PR 02-FEB-1994; 94DK-00000140.
XX PA (NOVO) NOVO-NORDISK AS.
XX PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;
XX WPI; 1995-161790/21.
XX PT New Bacillus derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
XX PS Disclosure; Page 75-76; 105pp; English.
XX CC Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability; low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 478 AA;
Query Match 95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 1.9e-216;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 ATPADWRSQSIYFLTLDRFARTDGGTTATCNTADOKYCGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLTLDRFARTDGGTTATCNTADOKYCGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTALPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLVVDVVA 140
DB 61 WITPVTALPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLVVDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTQVDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTQVDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240

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QY 261 PYQVMDGVLNPIYYPLLNAPKSTSGSMDDLYNMINTVKSDCPDSTLLGTTFVENHNDPR 320
DB 241 PYQVMDGVLNPIYYPLLNAPKSTSGSMDDLYNMINTVKSDCPDSTLLGTTFVENHNDPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGPIIYAGQCHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGPIIYAGQCHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 440
DB 361 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 420
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 5
AAR78270
ID AAR78270 standard; protein; 478 AA.
XX
AC AAR78270;
XX
DT 17-JAN-1996 (first entry)
XX
DE Aspergillus oryzae alpha amylase (mature protein).
XX
KW Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
KW thermostable; methionine; Bacillus licheniformis;
KW Bacillus amyloliquefaciens; Bacillus stearothermophilus;
KW Aspergillus oryzae.
XX
OS Aspergillus oryzae.
XX
FN WO9521247-A1.
XX
PD 10-AUG-1995.
XX
PF 05-OCT-1994; 94WO-DK000371.
XX
PR 02-FEB-1994; 94DK-00000141.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Toft AH, Marcher D, Pedersen HH, Nilsson TE;
XX
DR WPI; 1995-283767/37.
XX
PT Use of an oxidation stable alpha-amylase - for simultaneous desizing and
PT bleaching or scouring of fabrics contg. starch or starch derivs.
XX
PS Disclosure; Page 25-26; 37pp; English.
XX
CC Oxidation stable alpha amylases can be used for the simultaneous desizing
CC and bleaching or scouring of a fabric comprising starch or starch
CC derivatives. They exhibit a better heat stability, especially in the
CC presence of oxidising agents. They are obtained from a parent alpha
CC amylase by replacing one or more methionine residues with any amino acid
CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
CC Asp. The parent alpha amylase is pref. derived from a Bacillus species,
CC although alpha amylases of fungal origin can also be used. This sequence
CC is the wild type (unmodified) alpha amylase of Aspergillus oryzae
XX
XX Sequence 478 AA;
XX
Query Match 95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 1.9e-216;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 ATPADWRSQSISYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDYIQMGFTAI 80
DB 1 ATPADWRSQSISYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDYIQMGFTAI 60

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QY 81 WITPVTALPOTTAYGDAYHGYWQODIYSLNENYCTADDLKALSSALHERGMYLMDVVA 140
DB 61 WITPVTALPOTTAYGDAYHGYWQODIYSLNENYCTADDLKALSSALHERGMYLMDVVA 120
QY 141 NHMGYDGAGSSVDYSVFKPFSQDYFHPFCFTQNYEDQTVQVEDCWLGONTVSLPDLDTTK 200
DB 121 NHMGYDGAGSSVDYSVFKPFSQDYFHPFCFTQNYEDQTVQVEDCWLGONTVSLPDLDTTK 180
QY 201 DVVKNEWYDWVGSLSVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 260
DB 181 DVVKNEWYDWVGSLSVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTC 240
QY 261 PYQVMDGVLNPIYYPLLNAPKSTSGSMDDLYNMINTVKSDCPDSTLLGTTFVENHNDPR 320
DB 241 PYQVMDGVLNPIYYPLLNAPKSTSGSMDDLYNMINTVKSDCPDSTLLGTTFVENHNDPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGPIIYAGQCHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGPIIYAGQCHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 440
DB 361 LIASANAIRNYAISKDTGFTVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 420
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 6
AAW14500
ID AAW14500 standard; protein; 478 AA.
XX
AC AAW14500;
XX
DT 04-JUN-1997 (first entry)
XX
DE Aspergillus oryzae alpha-amylase (mature protein).
XX
KW alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
KW Aspergillus oryzae; Bacillus amyloliquefaciens; altered property;
KW calcium dependency; substrate binding; stability; pH optimum;
KW thermostability; cleavage; oligosaccharide substrate; dishwashing;
KW washing; detergent additive; fabric desizing; starch liquefaction;
KW sweetener; ethanol production; variant.
XX
OS Aspergillus oryzae.
XX
FH Key Location/Qualifiers
FT Misc-difference 13..45
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 7-23 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 33"
FT Misc-difference 14..40
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 8-18 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 35"
FT Misc-difference 28..42
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT Misc-difference 32..38
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for

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a variant) corresponding to 14-15 of AAW14499 is deleted
or replaced with a fragment corresponding to this
fragment; claim 32"
Misc-difference 66. .84
/label= loop 2 modification region
/note= "at least one amino acid residue of a parent alpha
-amyase (used as a template for a variant) corresponding
to 44-57 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 18"
Misc-difference 70. .78
/label= loop 2 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amyase (used as a template for
a variant) corresponding to 48-51 of AAW14499 is deleted
or replaced with a fragment corresponding to this
fragment; claim 20"
Misc-difference 98. .210
/label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha
-amyase (used as a template for a variant) corresponding
to 117-185 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 24"
Misc-difference 102. .206
/label= loop 3 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amyase (used as a template for
a variant) corresponding to 121-181 of AAW14499 is
deleted or replaced with a fragment corresponding to this
fragment; claim 26"
Misc-difference 121. .181
/note= "at least one amino acid residue of a parent alpha
-amyase (used as a template for a variant) corresponding
to this fragment is deleted or replaced with a fragment
corresponding to 102-206 of AAW14499; claim 41"
Misc-difference 121. .174
/note= "preferred region where at least one amino acid
residue of a parent alpha-amyase (used as a template for
a variant) corresponding to this fragment is deleted or
replaced with a fragment corresponding to 102-199 of
AAW14499; claim 42"
Misc-difference 165. .177
/label= loop 3 modification region
/note= "at least one amino acid residue of a parent alpha
-amyase (used as a template for a variant) corresponding
to 195-202 of AAW14499 is deleted or replaced with a
fragment corresponding to this fragment; claim 21"
Misc-difference 166. .173
/label= loop 3 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amyase (used as a template for
a variant) corresponding to 196-198 of AAW14499 is
deleted or replaced with a fragment corresponding to this
fragment; claim 23"
Misc-difference 181. .184
/note= "an amino acid fragment corresponding to this
region is deleted from the parent sequence of a variant
Fungamy1; claim 43"
Misc-difference 291. .313
/label= loop 8 modification region
/note= "at least one amino acid residue of a parent alpha
-amyase (used as a template for a variant) corresponding
to 322-346 of AAW14498 is deleted or replaced with a
fragment corresponding to this fragment; claim 36"
Misc-difference 297. .313
/label= loop 8 modification region
/note= "preferred region where at least one amino acid
residue of a parent alpha-amyase (used as a template for
a variant) corresponding to 325-345 of AAW14498 is
deleted or replaced with a fragment corresponding to this
fragment; claim 38"

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WO9623874-A1.

PD		08-AUG-1996.	
XX			
PF		05-FEB-1996;	96WO-DK000057.
XX			
PR		03-FEB-1995;	95DK-00000128.
PR		23-OCT-1995;	95DK-00001192.
PR		10-NOV-1995;	95DK-00001256.
XX			
PA		(NOVO) NOVO-NORDISK AS.	
XX			
PI	Svendsen A,	Bisgard-Frantzen H,	Borchert TV;
XX			
DR		WPI; 1996-371424/37.	
XX			
PT	Alpha-amylase variants and methods of production - have altered		
PT	properties such as calcium dependency, substrate binding and stability.		
XX			
PS	Disclosure; Page 87-88, 17lpp; English.		
XX			
CC	The present sequence is the mature Aspergillus oryzae alpha-amylase (A).		
CC	Variants of patent termamyl- and fungamyl-like alpha-amylases (and		
CC	methods of constructing them) are claimed. Examples of variants are		
CC	featured above. The variants have altered properties such as calcium		
CC	dependency, substrate binding and stability. Also one or more proline or		
CC	cysteine residues in the variant is modified or replaced with a non-		
CC	proline or non-cystein residue such as alanine. The variants can be used		
CC	for (dish)washing, as detergent additives or for fabric desizing or		
CC	starch liquefaction. They can also be used for the production of		
CC	sweeteners and ethanol from starch. See also AAW14498-99		
XX			
SQ	Sequence 478 AA;		
Query Match		95.8%;	Score 2572; DB 2; Length 478;
Best Local Similarity		99.8%;	Pred. No. 1.9e-216;
Matches 477; Conservative		0;	Mismatches 1; Indels 0; Gaps 0;
Qy	21	ATPADWRSSQIYFLLTDRPARTGSTTATCNTADQKYCGGTWGIIDKLDYIQMGFTAI	80
Dd	1	ATPADWRSSQIYFLLTDRPARTGSTTATCNTADQKYCGGTWGIIDKLDYIQMGFTAI	60
Qy	81	WIPTVTQAQLPQTAYGDVGHGYWQDIYSLNENYGTTADDLKALSSALHERGMYLMVDVVA	140
Dd	61	WIPTVTQAQLPQTAYGDVGHGYWQDIYSLNENYGTTADDLKALSSALHERGMYLMVDVVA	120
Qy	141	NHMGYDGAGSSVDYVFKEPSSQDYFHFPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK	200
Dd	121	NHMGYDGAGSSVDYVFKEPSSQDYFHFPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK	180
Qy	201	DVVKNEMYDWGSLVSNYSIDGLRIDTVKHVKDQFWPGYNKAAGVYCIGEVLDGDPAYTC	260
Dd	181	DVVKNEMYDWGSLVSNYSIDGLRIDTVKHVKDQFWPGYNKAAGVYCIGEVLDGDPAYTC	240
Qy	261	PYQNVMDGVNLNPIYPYPLNAFKSTSGSMDLNNMINTVKSDCPDSTLLGTFVENHDNPR	320
Dd	241	PYQNVMDGVNLNPIYPYPLNAFKSTSGSMDLNNMINTVKSDCPDSTLLGTFVENHDNPR	300
Qy	321	FASVTYNDIALAKNVAAFIILNDGIPITYAGOEQHYAGGNDDPANREATTWSGYPTDSLYK	380
Dd	301	FASVTYNDIALAKNVAAFIILNDGIPITYAGOEQHYAGGNDDPANREATTWSGYPTDSLYK	360
Qy	381	LIASANAIRNYAISKDTGFVYYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT	440
Dd	361	LIASANAIRNYAISKDTGFVYYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT	420
Qy	441	LSLSGAGYTAGOOLTEVIGCTTVTVSGDGNVPVMAGGLPRVLPTYPEKLAGSKICSSS	498
Dd	421	LSLSGAGYTAGOOLTEVIGCTTVTVSGDGNVPVMAGGLPRVLPTYPEKLAGSKICSSS	478
RESULT 7			
ABP96630			
ID ABP96630 standard; protein; 1095 AA.			
XX			

[illegible]

RESULT 9	
AAR79025	
ID	AAR79025 standard; protein; 478 AA.
XX	
XX	AAR79025;
XX	
XX	
DT	22-MAR-1996 (first entry)
XX	
XX	
DE	Mature taka-amylase A.
DE	
XX	
KW	Wild type; neopullulanase; B. stearothermophilus; mutant; food industry;
KW	modification; hydrophobicity; replacement insertion; deletion.
XX	
XX	
OS	Aspergillus oryzae.

Key	Location/Qualifiers
Disulfide-bond	30. .38
Disulfide-bond	150. .164
Disulfide-bond	240. .283
Disulfide-bond	439. .474
JP07177891-A.	
18-JUL-1995.	
31-OCT-1994;	94JP-00288658.
12-NOV-1993;	93JP-00306096.
(NIDE) NEC CORP. (EZAK) EZAKI GLICO CO.	
WPI; 1995-279919/37.	
Modifying a transferase by enhancing hydrophobicity of a selected site increases transfer activity, also new mutant neo-pullulanase(s).	
Disclosure; Page 10-11; 18pp; English.	

CC	This sequence represents the mature form of taka-amylase from <i>A. oryzae</i> .
CC	This sequence was used in a method for the generation of mutant
CC	pullulanases for use in the food industry (see also AAR79026-28). The
CC	wild type pullulanase enzyme was modified by the method of the invention
CC	for enhancing the hydrophobicity of a selected site of the pullulanase.
CC	The method comprises replacement of a group in the selected site with a
CC	hydrophobic group, replacement of an amino acid with a hydrophobic amino
CC	acid, and/or insertion or deletion of a hydrophobic amino acid from the
CC	selected site. The method was used to produce neopullulanases Y377F,
CC	S422V and M375L
XX	
SQ	Sequence 478 AA;
	Query Match 93.3%; Score 2503.5; DB 2; Length 478;
	Best Local Similarity 97.9%; Pred. No. 2e-210;
	Matches 468; Conservative 1; Mismatches 8; Indels 1; Gaps 1;
Qy	21 ATPADWRSSISIVPELLTDRFARTDGSATACNTADQKYCGGTWGGIIDKLDYIOGMGFTAI 80
Db	1 ATPADWRSSISIVPELLTDRFARTDGSATACNTADQKYCGGTWGGIIDKLDYIOGMGFTAI 60
Qy	81 WITPVTQAQLPQTAYGDAYGHYQQDIYSLNENYGTADDLKALSSALHERGMVLMVDVVA 140
Db	61 WITPVTQAQLPQDCAYGDAYTYWQTDIYSLNENYGTADDLKALSSALHERGMVLMVDVVA 120
Qy	141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 200
Db	121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK 180
Qy	201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGVLGDGPAYTC 260
Db	181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGVLGDGPAYTC 240
Qy	261 PYQNVMDGVLNYPPIYYPLNAPKSTSGSMDLLNMLNTVKSDCPDSTLLCTFFVENHDNPR 320
Db	241 PYQNVMDGVLNYPPIYYPLNAPKSTSGSMDLLNMLNTVKSDCPDSTLLCTFFVENHDNPR 300
Qy	321 FASYTYNDIALAKNVAAFIILNDGIPITTYAGQEQHYAGGNDPANREATWLSGYPTDSLYK 380
Db	301 FASYTYNDIALAKNVAAFIILNDGLPIIYAGQEQHYAGGNDPANREATWLSGYPTDSLYK 360
Qy	381 LIASANAIRNVAISKDTGFVYKNWPIYKDDTTIANRKGTGDSQIVTILSNKGASGDSYT 440
Db	361 LIASANAIRNVAISKDTGFVYKN- EYIKDDTTIANRKGTGDSQIVTILSNKGASGDSYT 419
Qy	441 LSLSGASYTAGOQLTEVIGCTTTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db	420 LSLSGASYTAGOQLTEVIGCTTTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSDS 477
RESULT 10	
ABB09072	
ID	ABB09072 standard; protein; 423 AA.
XX	
XX	ABB09072;
XX	
DT	26-JUN-2002 (first entry)
XX	
DE	Aspergillus oryzae TAKA protein (TAA).
XX	
KW	Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
KW	protein co-ordinate data; 3 dimensional structure.
XX	
OS	Aspergillus oryzae.
XX	
PN	KR2001027418-A.
XX	
PD	06-APR-2001.
XX	
PF	09-SEP-1999; 99KR-00039130.
XX	
PR	09-SEP-1999; 99KR-00039130.
XX	

PA (POST-) POSTECH FOUND.
XX (SAMY-) SAMYANG GENEX CORP.
PI Kim TJ, Park GH;
XX WPI; 2001-534477/59.
DR Manufacturing maltogenic amylase having improved transglycosylation
XX activity, comprises using crystallization.
PT Disclosure; Page 188; 196pp; Korean.
XX
XX The present invention describes manufacturing maltogenic amylase (EC
CC 3.2.1.133) having improved transglycosylation activity, comprising using
CC crystallisation and the three dimensional structure of maltogenic
CC amylase. Manufacturing maltogenic amylase comprises the following steps:
CC (i) obtaining a gene of maltogenic amylase from *Thermus* sp. IM6501 (KCTC
CC 5027BP) and inserting the gene into plasmid pUC119 to construct
CC recombinant DNA (pThMA119); (ii) inserting the recombinant DNA to
CC *Escherichia coli* MC1061; (iii) which is cultivated at 37 plus degrees Celsius
CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
CC supernatant through column chromatography and obtaining purified
CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two
CC maltogenic amylase molecules, and a *Thermus* sp. IM6501 maltogenic amylase
CC (ThMA) crystal. The amylase has a structure containing an activated
CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
CC and a pocket with glucose bound that consists of amino acid residues of
CC Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn131, Glu132, Val1329,
CC and His1360. The present sequence represents *Aspergillus oryzae* TAKA
CC protein (TAA), given in comparison with ThMA in the present invention
XX
XX Sequence 423 AA;
SQ
Query Match 80.1%; Score 2151; DB 4; Length 423;
Best Local Similarity 95.7%; Pred. No. 1.4e-179;
Matches 405; Conservative 2; Mismatches 16; Indels 0; Gaps 0;
QY 25 DWRSSIVFLTDRTARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAIWITP 84
Db 1 DWRSSIVFLTDRTARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAIWITP 60
QY 85 VTAQLPQTAYGDVHGYWQDIYSLNENYGTADDLKALSSALHBERGMYLWVNVANHG 144
Db 61 VTAQLPQTAYGDVHGYWQDIYSLNENYGTADDLKALSSALHBERGMYLWVNVANHG 120
QY 145 YDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVQEDCWLGDNTVSLPDLDTTKDVVK 204
Db 121 YDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVQEDCWLGDNTVSLPDLDTTKDVVK 180
QY 205 NEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICGEVLDGDPAYTCPYQN 264
Db 181 NEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICGEVLDGDPAYTCPYQN 240
QY 265 VMDGVLYNPYYPLNNAFKSTSGMDDLNNMINTVSKDPCSTLLGTTFVHNHDPREASY 324
Db 241 VMDGVLYNPYYPLNNAFKSTSGMDDLNNMINTVSKDPCSTLLGTTFVHNHDPREASY 300
QY 325 TNDIALAKNVAFTIILNDGIPPIYAGQBQHYAGGNDPANREATWLSGYPTDSLYKLIAS 384
Db 301 TNDIALAKNVAFTIILNDGMPKIYWGQBQHYAGGNDPANREATWLSGYPTDSLYKLIAS 360
QY 385 ANAIRNVAISKDTGFTVYKNWPIYKYDDTTIARMKGTGDSQIVTILSNKGASGDSYTLIS 444
Db 361 ANAIRNVAISKDTGFTVYKNWPIYKYDDTTIARMKGTGDSQIVTILSNKGASGDSYTLIS 420
QY 445 GAG 447
Db 421 GAG 423
RESULT 11

ABB80177
ID ABB80177 standard; protein; 495 AA.
XX
AC ABB80177;
XX
DT 11-AUG-2003 (first entry)
XX
DE A. fumigatus AfAAL1.
XX
KW Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KW glyceride; starch; maltodextrin; oxidated phenolic compound;
KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KW textile; tea liquor; cleaning ability.
XX
OS *Aspergillus fumigatus*.
XX
PN WO2003012071-A2.
XX
PD 13-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024842.
XX
PR 03-AUG-2001; 2001US-0309870P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Jiang B, Storms R, Roemer T, Bussey H;
XX
DR WPI; 2003-332729/31.
DR N-PSDB; ABQ80345, ABQ80346.
XX
PT Novel isolated *Aspergillus fumigatus* polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.
XX
PS Claim 17; Page 134-35; 169pp; English.
XX
CC The sequences given in ABB80164-87 show enzymatic proteins derived from
CC A. fumigatus. These proteins display the catalytic activity of an enzyme
CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
CC galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrase or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC laccase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression

XX Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
 KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
 KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
 KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
 KW glyceride; starch; maltodextrin; oxidated phenolic compound;
 KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
 KW textile; tea liquor; cleaning ability.
 XX Aspergillus fumigatus.
 XX WO2003012071-A2.
 PN 13-FEB-2003.
 XX 05-AUG-2002; 2002WO-US024842.
 XX 03-AUG-2001; 2001US-0309870P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Jiang B, Storms R, Roemer T, Bussey H;
 XX N-PSDB; ABQ80347, ABQ80348.
 DR WPI; 2003-332729/31.
 XX Novel isolated Aspergillus fumigatus polypeptide, useful in various
 PT industries such as those involved in the making of food and feed,
 PT beverages, textiles and detergents.
 XX Claim 17; Page 139-40; 169pp; English.
 XX The sequences given in ABB80164-87 show enzymatic proteins derived from
 CC A. fumigatus. These proteins display the catalytic activity of an enzyme
 CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
 CC galactosidase, invertase, lipase, alpha-amylase, laccase,
 CC polygalacturonase or xylanase. Compositions comprising the tannase are
 CC useful for modulating the amount of compounds that comprise a gallate
 CC ester linkage in a composition. Compositions comprising cellulase are
 CC useful for modulating the amount of cellulose in a composition.
 CC Compositions comprising glucose oxidase are useful for modulating the
 CC amount of glucose or oxygen in a composition. Compositions comprising
 CC phytase are useful for modulating the amount of myo-inositol phosphates
 CC in a composition. Compositions comprising beta-galactosidase are useful
 CC for modulating the amount of lactose in a composition. Compositions
 CC comprising sucrose or invertase are useful for modulating the amount of
 CC sucrose in a composition. Compositions comprising lipase are useful for
 CC modulating the amount of glyceride in a composition. Compositions
 CC comprising alpha-amylases are useful for modulating the amount of
 CC starches or maltodextrins in a composition. Compositions comprising
 CC laccase are useful for modulating the amount of oxidated phenolic
 CC compounds in a composition. Compositions comprising polygalacturonases
 CC are useful for modulating the amount of high or low molecular weight
 CC polygalacturonic acid chains in a composition. Compositions comprising
 CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
 CC in a composition. The A. fumigatus proteins and corresponding DNA's are
 CC useful in various industries such as those involved in the making of food
 CC and feed, beverages, textiles and detergents. The DNA's are useful to
 CC express recombinant enzymes for characterization, modification or
 CC industrial uses, to compare with the nucleotide sequence of A. fumigatus
 CC to identify duplicated genes of paralogs having the same or similar
 CC biochemical activity and/or function, to compare with nucleic acid
 CC sequence of other related or distant fungal organisms to identify
 CC potential orthologous enzyme genes, for selecting and making oligomers
 CC for attachment to a nucleic acid array for examination of expression
 CC patterns, and to raise anti-protein antibodies. The polypeptide having
 CC tannase activity increases the yield of tea liquor from tea leaves,
 CC improves the colour, flavour and health benefits of tea products,
 CC particularly an instant tea product. The polypeptide having cellulase
 CC activity enhances cleaning ability of detergent compositions
 XX Sequence 630 AA;

Query Match 68.4%; Score 1835; DB 6; Length 630;
 Best Local Similarity 66.8%; Pred. No. 1.4e-151;
 Matches 334; Conservative 59; Mismatches 101; Indels 6; Gaps 2;
 QY 5 WSLFLYGLQVAAPAL-----AATPADMRSSQSIYFLLTDRFARTDGGTTATCNADQKCG 59
 Db 3 WISQFLPLSLCSLLGQAHAALTPAEMRSQSIYFLLTDRFGREDNSTTAACDVTQLYCG 62
 QY 60 GTWQGIIDLDYIQMGFTAIWTFVTAQLPQTAYGDAYHYGYWOODIYSLNENYGTADD 119
 Db 63 GSWQGIINHLDIQMGFTAIWTFVTEQFVENTGDTGTSYHYGYQONTHEVNANYGTAQD 122
 QY 120 LKALSSALHERGMYLMDVDVANHMGYDGAGSSVDYSVEKPFSSODYFHPFCFQIYNEQDT 179
 Db 123 LRDLANALHARGMYLMDVDVANHMGYDGAGSNVYGVETPDSATYFHPYCLITDYNQDT 182
 QY 180 QVEDCWLGDNVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGY 239
 Db 183 AVEDCWLGDVTVSLPDLDTTSTAVRSIWDVWVGLVANYSIDGLRIDTVKHVEKDFWPGY 242
 QY 240 NKAAGVYCVIGVLDGDPAYTCYQNVMDGVNLNRYPIYPLANAFKSTSGSMODLYNMINTV 299
 Db 243 NDAAGVYCVGVFGDPQYTCYQNYLDGVNLNRYPIYQOLLYAFPOSTSGISNLNMISSV 302
 QY 300 KSDCPDSTLLGTFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPITTYAGOEQHYAGCN 359
 Db 303 ASDCADPTLLGNFTENHNDNPRFASYTSDYSQAKNVISFMPFSDGIPITYAGOEQHYSGA 362
 QY 360 DPANREATWLSGYPTDSLYELKLIASANAIRNAYISKOTGFVYKNWPIYKDDTTIAMRKG 419
 Db 363 DPANREAVWLSGYSTSATLYSWIASTNKIRKLAISKDSAYITSKNPFYDSTNLAMRKG 422
 QY 420 T-DGSOIVTILSNKSGSDSYTSLSGAGYTAGOOLTEVIGCTTVCSDGNVPVPMAGG 478
 Db 423 SVAGSQVITVLSNKGSGSYTSLSGTGYGAGATLVEMYTCTLTITVDSSGNLAVPMVSG 482
 QY 479 LPRVLYPTEKLAGSKICSSS 498
 Db 483 LPRVFPSSWVSGSLCGDS 502
 RESULT 14
 AAE24207
 ID AAE24207 standard; protein; 484 AA.
 XX AAE24207;
 AC AAE24207;
 XX 04-OCT-2002 (first entry)
 DT Aspergillus niger alpha-amylase protein.
 DE Ethanol production; starch; fermentation; liquefaction; alpha-amylase;
 KW fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.
 XX Aspergillus niger.
 OS WO200238787-A2.
 PN 16-MAY-2002.
 PD 09-NOV-2001; 2001WO-DK000737.
 XX 10-NOV-2000; 2000DK-00001676.
 PR 21-NOV-2000; 2000US-0252213P.
 PR 11-DEC-2000; 2000DK-00001854.
 PR 15-DEC-2000; 2000US-0256015P.
 XX (NOVO) NOVOZYMES AS.
 PA (NOVO) NOVOZYMES NORTH AMERICA INC.
 XX Veit C, Felby C, Fuglsang CC;
 PI WPI; 2002-479793/51.
 DR

XX Producing ethanol from starch-containing material e.g., tubers, roots,
 PT whole grain, for use in fuel, by fermentation comprises carrying out a
 PT secondary liquefaction step in the presence of a thermostable acid alpha-
 PT amylase.
 XX
 XX Claim 35; Page 31-33; 33pp; English.
 XX
 XX The invention relates to a method for producing ethanol from starch-
 CC containing material, by fermentation. The method involves carrying out a
 CC secondary liquefaction step in the presence of a thermostable acid alpha-
 CC amylase. The method is used in producing ethanol from a starch-containing
 CC material such as tubers, roots or whole grain (e.g. corn, wheat or barley
 CC or their combination) or combination of the materials. Preferably ethanol
 CC is produced from starch-containing material that is obtained from cereals
 CC or from corns, cobs, wheat, barley, rye, milo and potatoes or their
 CC combination. The ethanol produced by above mentioned method is used as
 CC fuel alcohol and/or fuel additive. The ethanol is also useful as drinking
 CC ethanol i.e., potable neutral spirits or industrial ethanol. The present
 CC sequence is *Aspergillus niger* alpha-amylase protein
 XX
 XX Sequence 484 AA;

Query Match 66.2%; Score 1778; DB 5; Length 484;
 Best Local Similarity 66.9%; Pred. No. 9.1e-147;
 Matches 318; Conservative 63; Mismatches 94; Indels 0; Gaps 0;

QY 24 ADWRQSIVFLLTDRFARTDGTATCNTADQKYGCTWQGIIDKLDYIQGMFTAIWIT 83
 DB 4 ASWRTOSIVFLLTDRFRTDNTTATCNTGNEIYCGSGWQGIIDHLDYIEGSGFTAIWIS 63

QY 84 PVTAQLPQTAYGDAGHYGWQDIYSLNENYGTADDLKALSSALHARGMYLWVVDVPHM 143
 DB 64 PITEQLPQDTADGEAYHGWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVVDVPHM 123

QY 144 GYDAGSSVDYSVPKPFSSQDYFHPFCFQNYEDQTOVEDCWLGNTVSLPDLDTTKDV 203
 DB 124 GYAGNGNDVYSVPDPFSSSYFHPYCLITDNDLTMWEDCWEGDTIVSLPDLDTTETAV 183

QY 204 KNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGELVDGDPAYTCPYQ 263
 DB 184 RTIWDVADLVSNYSVDGLRIDSLEVPDPFPGYNKASGVYCVGEIDNGPASPDPYQ 243

QY 264 NVMDGVNLPIIYPLNAPKSTSGSMDLLNMINTVKSDCPDSTLLGTVEHNDNPRPAS 323
 DB 244 KVLGDVNLPIYQLLYAFESSSGSISNLNMIKSVASDCSDPTLLGNFIENHNDNPRFAK 303

QY 324 YTNDAALAKNVAAFIILNDGPIIYAGQHQYAGGNDPANREATWLSGYPTDSELYKLTIA 383
 DB 304 YTSYDQAKNVLISYIFLSDGPIVYAGEBQHYAGGKVPYNREATWLSGYDTSALYTWIA 363

QY 384 SANAIENYAIKSDTGFVTYKNWPIYKDDTTIAMRKGTGSGQIVITILSNKGASGDSYTL 443
 DB 364 TTNAIRKLAIAADSAYITANDAFYDTSNTIAMAKTSGSQVITVLSNKGSSSYTLTL 423

QY 444 SGAGYTAGQOLTEVIGCTTIVTGVSGDNVVPVPMAGGLPRVLYPTEKLAGSKICSS 498
 DB 424 SSGSYTSGTKLIEAYTCTSVTVDSGDIPVPMASGLPRVLLPASVVDSSSLCGS 478

RESULT 15
 ADS75939
 ID ADS75939 standard; protein; 484 AA.
 XX
 XX ADS75939;
 XX
 XX 16-DEC-2004 (first entry)
 DT
 XX
 XX *Aspergillus niger* acid alpha-amylase for ethanol production method.
 DE
 DE enzyme; alcohol; slurry; water; granular starch; acid alpha-amylase;
 KW glucoamylase; gelatinization; yeast; beer; fuel ethanol; potable ethanol;
 KW industrial ethanol.

XX *Aspergillus niger*.
 XX WO2004080923-A2.
 XX
 XX 23-SEP-2004.
 XX
 XX 10-MAR-2004; 2004WO-DK000154.
 XX
 XX 10-MAR-2003; 2003US-0453326P.
 XX
 XX (NOVO) NOVOZYMES AS.
 XX
 XX Olsen HS, Pedersen S, Festersen RM;
 XX WPI; 2004-677503/66.
 XX
 XX Production of alcohol product, e.g. beer, comprises holding slurry of
 PT water and granular starch in presence of acid alpha-amylase and
 PT glucoamylase followed by simultaneous saccharification and fermentation.
 XX
 XX Claim 9; SEQ ID NO 1; 43pp; English.
 XX
 XX The invention relates to a method for the production of an alcohol
 CC product by holding a slurry of water and granular starch in the presence
 CC of an acid alpha-amylase and a glucoamylase at 0-20 deg C below the
 CC initial gelatinization temperature of the granular starch; holding the
 CC slurry in the presence of acid alpha-amylase, glucoamylase and yeast at
 CC 10-35 deg C to produce ethanol; and optionally recovering the ethanol.
 CC The method is used for the production of an alcohol product such as beer
 CC or recovered ethanol, e.g. fuel ethanol, potable ethanol or industrial
 CC ethanol. This sequence represents an acid fungal alpha-amylase from
 CC *Aspergillus niger* used in the method of the invention.
 XX
 XX Sequence 484 AA;

Query Match 66.2%; Score 1778; DB 8; Length 484;
 Best Local Similarity 66.9%; Pred. No. 9.1e-147;
 Matches 318; Conservative 63; Mismatches 94; Indels 0; Gaps 0;

QY 24 ADWRQSIVFLLTDRFARTDGTATCNTADQKYGCTWQGIIDKLDYIQGMFTAIWIT 83
 DB 4 ASWRTOSIVFLLTDRFRTDNTTATCNTGNEIYCGSGWQGIIDHLDYIEGSGFTAIWIS 63

QY 84 PVTAQLPQTAYGDAGHYGWQDIYSLNENYGTADDLKALSSALHARGMYLWVVDVPHM 143
 DB 64 PITEQLPQDTADGEAYHGWQKIYDVNSNFGTADNLKSLSDALHARGMYLWVVDVPHM 123

QY 144 GYDAGSSVDYSVPKPFSSQDYFHPFCFQNYEDQTOVEDCWLGNTVSLPDLDTTKDV 203
 DB 124 GYAGNGNDVYSVPDPFSSSYFHPYCLITDNDLTMWEDCWEGDTIVSLPDLDTTETAV 183

QY 204 KNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGELVDGDPAYTCPYQ 263
 DB 184 RTIWDVADLVSNYSVDGLRIDSLEVPDPFPGYNKASGVYCVGEIDNGPASPDPYQ 243

QY 264 NVMDGVNLPIIYPLNAPKSTSGSMDLLNMINTVKSDCPDSTLLGTVEHNDNPRPAS 323
 DB 244 KVLGDVNLPIYQLLYAFESSSGSISNLNMIKSVASDCSDPTLLGNFIENHNDNPRFAK 303

QY 324 YTNDAALAKNVAAFIILNDGPIIYAGQHQYAGGNDPANREATWLSGYPTDSELYKLTIA 383
 DB 304 YTSYDQAKNVLISYIFLSDGPIVYAGEBQHYAGGKVPYNREATWLSGYDTSALYTWIA 363

QY 384 SANAIENYAIKSDTGFVTYKNWPIYKDDTTIAMRKGTGSGQIVITILSNKGASGDSYTL 443
 DB 364 TTNAIRKLAIAADSAYITANDAFYDTSNTIAMAKTSGSQVITVLSNKGSSSYTLTL 423

QY 444 SGAGYTAGQOLTEVIGCTTIVTGVSGDNVVPVPMAGGLPRVLYPTEKLAGSKICSS 498
 DB 424 SSGSYTSGTKLIEAYTCTSVTVDSGDIPVPMASGLPRVLLPASVVDSSSLCGS 478

Search completed: November 7, 2005, 18:57:39
Job time : 295.301 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:40:32 ; Search time 57.6834 Seconds
(without alignments)
830.671 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 2684
Sequence: 1 MVAWSLFYGLQVAPALAA.....LPRVLYPTEKLAGSKICSSS 498
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2684	100.0	499	1 ALAS1	alpha-amylase (EC
2	2675	99.7	499	2 JS0663	alpha-amylase (EC
3	2674	99.6	499	1 ALAS3	alpha-amylase (EC
4	2674	99.6	499	2 B43305	alpha-amylase (EC
5	2673	99.6	499	2 JN0588	alpha-amylase (EC
6	2662	99.2	498	2 A48305	alpha-amylase (EC
7	2656	99.0	498	2 J70466	alpha-amylase (EC
8	2503.5	93.3	478	2 JK0201	alpha-amylase (EC
9	1780	66.7	484	1 A35282	alpha-amylase (EC
10	1629	60.7	624	1 JC4510	pullulanase (EC 3.
11	1527	56.9	507	2 S33921	alpha-amylase (EC
12	1449	54.0	512	2 S06115	alpha-amylase (EC
13	1445.5	53.9	512	2 S23355	alpha-amylase (EC
14	1397.5	52.1	494	1 ALBYAF	alpha-amylase (EC
15	1264	47.1	631	2 S72270	alpha-amylase (EC
16	1015.5	37.8	513	2 T38770	alpha-amylase a pr
17	963.5	35.9	625	2 T41603	alpha-amylase - fi
18	920.5	34.3	491	2 T38448	probable alpha-am
19	899	33.5	581	2 S62505	probable alpha-am
20	898.5	33.5	564	2 T41503	alpha-amylase - fi
21	898	33.5	478	2 T40860	probable alpha-am
22	737	27.5	482	2 S34478	alpha-amylase (EC
23	670	25.0	1196	2 A29130	beta-amylase (EC 3
24	653.5	24.3	774	2 T39539	alpha-amylase homo
25	481.5	17.9	642	2 AL1827	cyclomaltodextrin
26	456.5	17.0	713	1 ALBSG1	cyclomaltodextrin
27	454.5	16.9	712	1 ALBSG3	cyclomaltodextrin
28	444.5	16.6	713	1 ALBSG7	cyclomaltodextrin
29	440.5	16.4	528	1 ALBSK	alpha-amylase (EC

ALIGNMENTS

RESULT 1

ALAS1

alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae

N:Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A

C:Species: Aspergillus oryzae

C>Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004

C:Accession: S04548; A33214; JS0240; A91930; A93767; A10627

R:Wirsal, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A:Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon

A:Reference number: S04548; MUID:89237897; PMID:2785629

A:Accession: S04548

A:Molecule type: DNA

A:Residues: 1-499 <WIR>

A:Cross-references: UNIPROT:P10529; EMBL:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

A:Genetics: AMY1

A:Accession: A33214

A:Molecule type: mRNA

A:Residues: 1-499 <W12>

A:Cross-references: GB:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

R:Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989

A:Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin

A:Reference number: JS0240; MUID:89378767; PMID:2789162

A:Accession: JS0240

A:Molecule type: DNA

A:Residues: 1-499 <GEN>

A:Genetics: AMY2

A:Note: the authors refer to this as isozyme II

R:Isemura, S.; Ikenaka, T.

J. Biochem. 74, 1-10, 1973

A:Reference number: A91930; MUID:74001521; PMID:4733850

A:Accession: A91930

A:Molecule type: protein

A:Residues: 206-225 <ISE>

R:Narita, K.

Proc. Jpn. Acad. 51, 285-290, 1975

A:Reference number: A93767

A:Accession: A93767

A:Molecule type: protein

A:Residues: 434-443,446-447, 'O', 449-458, 'GRTV', 459-464,467-468, 'B', 470, 'B', 472-499 <NAR

R:Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A:Title: Structure and possible catalytic residues of Taka-amylase A.

A:Reference number: A37454; MUID:84212370; PMID:6609921

A:Contents: annotation; X-ray crystallography, 3.0 angstroms

R:Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkmenburg, J.P.; Wilkinson, A.

submitted to the Brookhaven Protein Data Bank, August 1992

A:Reference number: A51548; PDB:6TAA

A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497

C:Comment: One atom of calcium per molecule is essential for activity.

C:Genetics: <AMY1>

A:Gene: amy1
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Genetics: <AMY2>
A:Gene: amy2; AmyII
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <Sig>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F:142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2684; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 7e-185;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVAWNSFLYGLQVAAPALAAPADWRQSQSYIFLLTDRPARTDGSSTTATCNTADQKCGG 60
Db 2 MVAWNSFLYGLQVAAPALAAPADWRQSQSYIFLLTDRPARTDGSSTTATCNTADQKCGG 61

Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 121

Qy 121 KALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
Db 122 KALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181

Qy 181 VEDCWLGNDTSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240
Db 182 VEDCWLGNDTSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 241

Qy 241 KAAGVYCIGEVLGDGPAYTCPYQNMVGLNYPYIYPLNAPFKSTGSMDDLNNINTVK 300
Db 242 KAAGVYCIGEVLGDGPAYTCPYQNMVGLNYPYIYPLNAPFKSTGSMDDLNNINTVK 301

Qy 301 SDCPDSTLLGTFVENHNDPRFASVTNDIALAKNVAFAFIILNDGPIIYAGQEHYAGGND 360
Db 302 SDCPDSTLLGTFVENHNDPRFASVTNDIALAKNVAFAFIILNDGPIIYAGQEHYAGGND 361

Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRKG 420
Db 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRKG 421

Qy 421 DGSQIVTILSNKGASGDSYITLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480
Db 422 DGSQIVTILSNKGASGDSYITLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

Qy 481 RVLYPTEKLAGSKICSSS 498
Db 482 RVLYPTEKLAGSKICSSS 499

RESULT 2
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C:Species: Aspergillus sp.
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C:Accession: JS0663
R:Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A:Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyamae and its expression
A:Reference number: JS0663; MUID:92323146; PMID:1368777
A:Accession: JS0663
A:Molecule type: mRNA
A:Residues: 1-499 <SHI>
C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <Sig>
F:22-499/Product: alpha-amylase #status predicted <ALP>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.7%; Score 2675; DB 2; Length 499;
Best Local Similarity 99.8%; Pred. No. 3.1e-184;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVAWNSFLYGLQVAAPALAAPADWRQSQSYIFLLTDRPARTDGSSTTATCNTADQKCGG 60
Db 2 MVAWNSFLYGLQVAAPALAAPADWRQSQSYIFLLTDRPARTDGSSTTATCNTADQKCGG 61

Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 121

Qy 121 KALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
Db 122 KALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181

Qy 181 VEDCWLGNDTSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240
Db 182 VEDCWLGNDTSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 241

Qy 241 KAAGVYCIGEVLGDGPAYTCPYQNMVGLNYPYIYPLNAPFKSTGSMDDLNNINTVK 300
Db 242 KAAGVYCIGEVLGDGPAYTCPYQNMVGLNYPYIYPLNAPFKSTGSMDDLNNINTVK 301

Qy 301 SDCPDSTLLGTFVENHNDPRFASVTNDIALAKNVAFAFIILNDGPIIYAGQEHYAGGND 360
Db 302 SDCPDSTLLGTFVENHNDPRFASVTNDIALAKNVAFAFIILNDGPIIYAGQEHYAGGND 361

Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRKG 420
Db 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKKNWPIYKDDTTIAMRKG 421

Qy 421 DGSQIVTILSNKGASGDSYITLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480
Db 422 DGSQIVTILSNKGASGDSYITLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

Qy 481 RVLYPTEKLAGSKICSSS 498
Db 482 RVLYPTEKLAGSKICSSS 499

RESULT 3
ALAS3
alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N:Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S04549; A33215; A44713
R:Wiesel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A:Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon o
A:Reference number: S04548; MUID:89237897; PMID:2785629
A:Accession: S04549
A:Molecule type: DNA
A:Residues: 1-499 <WIR>
A:Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922
A:Accession: A33215
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-499 <WIR>
A:Cross-references: CB:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922
R:Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A:Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing

A:Reference number: JS0240; MUID:89378767; PMID:2789162

A:Accession: A44713

A:Molecule type: DNA

A:Residues: 1-499 <GEN>

A:Note: the authors refer to this as isozyme I

R:Matuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A:Title: Structure and possible catalytic residues of Taka-amylase A.

A:Reference number: A37454; MUID:84212370; PMID:6609921

A:Contents: annotation; X-ray crystallography, 3.0 angstroms

C:Comment: One atom of calcium per molecule is essential for activity.

C:Genetics:

A:Gene: amy3; AmyI

A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; metal

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-499/Product: alpha-amylase 3 #status experimental <MAT>

F:194-321/Domain: alpha-amylase core homology <AMY>

F:51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental

F:142,183,196,231/Binding site: calcium (Asn, Glu, His) #status predicted

F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 99.6%; Score 2674; DB 1; Length 499;

Best Local Similarity 99.6%; Pred. No. 3.7e-184;

Matches 496; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKYCGG 60

DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKYCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHGYWQDDIYSLNENYGTADDL 120

DB 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHGYWQDDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMYLWVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQIQ 180

DB 122 KALSSALHERGMYLWVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQIQ 181

QY 181 VEDCWLGNTVSLPDLDTTKOVVKNWYDVGSLVSNYSIDGLRIDTVKHVKDFWPGYN 240

DB 182 VEDCWLGNTVSLPDLDTTKOVVKNWYDVGSLVSNYSIDGLRIDTVKHVKDFWPGYN 241

QY 241 KAAGVYICGEVLDDGDPAYTCPQNVMDGVLNPIYYPPLNAPKSTSGSMDLLYNMINTVK 300

DB 242 KAAGVYICGEVLDDGDPAYTCPQNVMDGVLNPIYYPPLNAPKSTSGSMDLLYNMINTVK 301

QY 301 SDPCDSTLLGTVEVNDHNPFRASYTNDIALAKNVAFIILNDGIPILYAGQEHYAGGND 360

DB 302 SDPCDSTLLGTVEVNDHNPFRASYTNDIALAKNVAFIILNDGIPILYAGQEHYAGGND 361

QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVTKNWPFIYKDDTTIAMRKGT 420

DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVTKNWPFIYKDDTTIAMRKGT 421

QY 421 DGSQIVTILSNKAGSDSYTLISGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480

DB 422 DGSQIVTILSNKAGSDSYTLISGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

QY 481 RVLYPTEKLAGSKICSSS 498

DB 482 RVLYPTEKLAGSKICSSS 499

RESULT 5

JN0588

alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae

N:Alternate names: Taka-amylase A

C:Species: Aspergillus oryzae

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: JN0588

R:Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kirita, N.; Teuboi, A.; Uda, S.

Gene 84, 319-327, 1989

A:Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m

A:Reference number: JN0588; MUID:90128276; PMID:2612911

A:Accession: JN0588

A:Molecule type: mRNA

A:Residues: 1-499 <TSU>

A:Cross-references: UNIPROT:Q96TH4

RESULT 4

B48305

alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori

C:Species: Aspergillus awamori

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Comment: The alpha amylases are encoded by multigene family.

C;Genetics:

A;Gene: Taa-G1

A;Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-499/Product: alpha-amylase #status predicted <NAT>

F;194-321/Domain: alpha-amylase core homology <AMY>

F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.6%; Score 2673; DB 2; Length 499;

Best Local Similarity 99.6%; Pred. No. 4.3e-184;

Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGG 60

DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDVHGQYQODIYSLNENYGTADDL 120

DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDVHGQYQODIYSLNENYGTADDL 121

QY 121 KALSSALHERGMVLMVDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180

DB 122 KALSSALHERGMVLMVDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181

QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPQYN 240

DB 182 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPQYN 241

QY 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLPIYPLNAPKSTSGMDDLNNINTVK 300

DB 242 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLPIYPLNAPKSTSGMDDLNNINTVK 301

QY 301 SDPCPSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIINDGIPILYAGQEHYAGGND 360

DB 302 SDPCPSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIINDGIPILYAGQEHYAGGND 361

QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKMWPIYKDDTTIAMRKT 420

DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKMWPIYKDDTTIAMRKT 421

QY 421 DGSQVITILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480

DB 422 DGSQVITILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

QY 481 RVLVPTKLAGSKICSSS 498

DB 482 RVLVPTKLAGSKICSSS 499

RESULT 6

A48305

alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori

C;Species: Aspergillus awamori

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: A48305

R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;

Curr. Genet. 17, 203-212, 1990

A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper

A;Reference number: A48305; PMID:90254827; PMID:2340591

A;Accession: A48305

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-498 <KOR>

A;Cross-references: UNIPROT:Q02905

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 99.2%; Score 2662; DB 2; Length 498;

Best Local Similarity 99.6%; Pred. No. 2.7e-183;

Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGG 60

DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDVHGQYQODIYSLNENYGTADDL 120

DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDVHGQYQODIYSLNENYGTADDL 121

QY 121 KALSSALHERGMVLMVDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180

DB 122 KALSSALHERGMVLMVDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181

QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPQYN 240

DB 182 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPQYN 241

QY 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLPIYPLNAPKSTSGMDDLNNINTVK 300

DB 242 KAAGVYCI GEVLGDGPAYTCYQNVMDGVNLPIYPLNAPKSTSGMDDLNNINTVK 301

QY 301 SDPCPSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIINDGIPILYAGQEHYAGGND 360

DB 302 SDPCPSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIINDGIPILYAGQEHYAGGND 361

QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKMWPIYKDDTTIAMRKT 420

DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKMWPIYKDDTTIAMRKT 421

QY 421 DGSQVITILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480

DB 422 DGSQVITILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

QY 481 RVLVPTKLAGSKIC 495

DB 482 RVLVPTKLAGSKIC 496

RESULT 7

UT0466

alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae

N;Alternate names: glycogenase; Taka-amylase A

C;Species: Aspergillus oryzae

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C;Accession: JT0466

R;Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.

Agric. Biol. Chem. 53, 593-599, 1989

A;Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill

A;Reference number: JT0466

A;Accession: JT0466

A;Molecule type: DNA

A;Residues: 1-499 <TAD>

A;Cross-references: UNIPROT:P10529

C;Comment: See also PIR:JK0201 and PIR:JSQ240.

C;Comment: One atom of calcium per molecule is essential for activity.

C;Genetics:

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-499/Product: alpha-amylase #status predicted <NAT>

F;194-321/Domain: alpha-amylase core homology <AMY>

F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:231,251,318/Active site: His, Glu, Asp #status predicted

Query Match 99.0%; Score 2656; DB 2; Length 499;
Best Local Similarity 99.4%; Pred. No. 7.2e-183;
Matches 495; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 MVAWSEFLYGLQVAAPALAAATPADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGG 60
DB 2 MVAWSEFLYGLQVAAPALAAATPADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGG 61

QY 61 TWQGIIDKLDYIOGMGFTAIWTPVTAQPLQTTAYGDVHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIOGMGFTAIWTPVTAQPLQTTAYGDVHGYWQDIYSLNENYGTADDL 121

QY 121 KALSSALHBERGMYLMDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQ 180
DB 122 KALSSALHBERGMYLMDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQ 181

QY 181 VEDCWLGDNVSLPDLDTTKDVVKNENYDWVGLSVNSYIDGLRIDTVKHVQKDFWPGYN 240
DB 182 VEYCWLGDNVSLPDLDTTKDVVKNENYDWVGLSVNSYIDGLRIDTVKHVQKDFWPGYN 241

QY 241 KAAGVYICIGEVLDGDPAYTCFYQNVMDGVLYNYPIYYPLNAPKSTSGSMDLLYNMINTVK 300
DB 242 KAAGVYICIGEVLDGDPAYTCFYQNVMDGVLYNYPIYYPLNAPKSTSGSMDLLYNMINTVK 301

QY 301 SDPCDSTLLGTGFVENHNDNPRFASYTNDIALAKNVAAFIILNDGPIIYAGQBOHYAGND 360
DB 302 SDPCDSTLLGTGFVENHNDNPRFASYTNDIALAKNVAAFIILNDGPIIYAGQBOHYAGND 361

QY 361 PANREATWLSGYPTDSELYKLATASANAIRNYAISKDTGFVYKQWPIYKDDTTIAMRKGT 420
DB 362 PANREATWLSGYPTDSELYKLATASANAIRNYAISKDTGFVYKQWPIYKDDTTIAMRKGT 421

QY 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGOOLTEVIGCTTVTVGSDGNVPPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLISLGAGYTAGOOLTEVIGCTTVTVGSDGNVPPVPMAGGLP 481

QY 481 RVLYPEKLAGSKICSSS 498
DB 482 RVLYPEKLAGSKICSSS 499
```

RESULT 8

JK0201
alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
N:Alternate names: glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
R:Toda, H.; Kondo, K.; Narita, K.
Proc. Jpn. Acad. 58B, 208-212, 1982
A:Title: The complete amino acid sequence of Taka-amylase A.
A:Reference number: JK0201
A:Accession: JK0201
A:Molecule type: protein
A:Residues: 1-478 <TOD>
A:Cross-references: UNIPROT:P10529
C:Comment: One atom of calcium per molecule is essential for the activity.
C:Comment: This enzyme is a glycoprotein.
C:Comment: See also PIR:J70466 and PIR:JS0240.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domain: alpha-amylase core homology <AMY>
F:197/Binding site: carboxylate (Asn) (covalent) #status experimental
F:210,230,297/Active site: His, Glu, Asp #status experimental

Query Match 93.3%; Score 2503.5; DB 2; Length 478;
Best Local Similarity 97.9%; Pred. No. 5.9e-172;
Matches 468; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

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QY 21 ATPADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAI 80
DB 1 ATPADWRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAI 60

QY 81 WITPVTQAQLPQTTAYGDVHGYWQDIYSLNENYGTADDLKALSSALHBERGMYLMDVNV 140
DB 61 WITPVTQAQLPQTTAYGDVHGYWQDIYSLNENYGTADDLKALSSALHBERGMYLMDVNV 120

QY 141 NEMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNVSLPDLDTTK 200
DB 121 NEMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNVSLPDLDTTK 180

QY 201 DVVKNENYDWVGLSVNSYIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNENYDWVGLSVNSYIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240

QY 261 PYQNVMDGVLYNYPIYYPLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTGFVENHNDN 320
DB 241 PYQNVMDGVLYNYPIYYPLNAPKSTSGSMDLLYNMINTVKSDCPDSTLLGTGFVENHNDN 300

QY 321 FASYTNDIALAKNVAAFIILNDGPIIYAGQBOHYAGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGPIIYAGQBOHYAGNDPANREATWLSGYPTDSELYK 360

QY 381 LIASANAIRNYAISKDTGFVYKQWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSY 440
DB 361 LIASANAIRNYAISKDTGFVYKQWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSY 419

QY 441 LSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPPVPMAGGLPRLVLYPTEKLAGSKICSS 498
DB 420 LSLSGAGYTAGOOLTEVIGCTTVTVGSDGNVPPVPMAGGLPRLVLYPTEKLAGSKICSDS 477
```

RESULT 9

A35282
alpha-amylase (EC 3.2.1.1) - Aspergillus niger
C:Species: Aspergillus niger
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: A35282
R:Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pet
Biochemistry 29, 6244-6249, 1990
A:Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom
A:Reference number: A35282; PMID:91002514; PMID:2207069
A:Accession: A35282
A:Molecule type: mRNA
A:Residues: 1-484 <BOE>
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domain: alpha-amylase core homology <AMY>

Query Match 66.3%; Score 1780; DB 1; Length 484;
Best Local Similarity 67.2%; Pred. No. 5.1e-120;
Matches 319; Conservative 63; Mismatches 93; Indels 0; Gaps 0;

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QY 24 ADMRSOSIYFLLTDRFARTDGSSTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAIWIT 83
DB 4 AEMRTOSIYFLLTDRFARTDGSSTATCNTADQKYCGGTWQGIIDKLDYIOGMGFTAIWIS 63

QY 84 PVTQAQLPQTTAYGDVHGYWQDIYSLNENYGTADDLKALSSALHBERGMYLMDVNVANHM 143
DB 64 PITEQLPQTTADGEAHVGYWQDIYDVNSNFTADDLSLSDALHARGMYLMDVNVANHM 123

QY 144 GYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNVSLPDLDTTKDV 203
DB 124 GYAGNDVDYSVFPDFDSSSYFHPYCLITDNLTMVQDCWEGDITVSLPDLNLTETAV 183

QY 204 KNEWMDVGLSVNSYIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 263
```

Db 184 RTIWDVADLVSNYSVDGLRIDSVLEVPDFPPQYQEAAGVYCVGEVDNGNPAIDCPYQ 243

QY 264 NVMDGVLNYPPIYPLINAFKSTSGSMDLYNNMTVKSDCPDSTLLGTVEHNDNPRFAS 323

Db 244 KVLGDVLNPTTWQLLYAFESSGSLNLYNMIXVASDCSDPTLLGNFIENHNDNPRFAS 303

QY 324 YTNIDIALAKNVAAFIILNDGIPPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYKLTA 383

Db 304 YTSDSYQAQNVLSYIFLSGPIPIVYAGEBQHYSGGKVPYNREATWLSGYDTSAEIYTWTIA 363

QY 384 SANATRYNAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKAGSDSYTSL 443

Db 364 TTNARKLAISADSAITYANDAFYDTSNTIAMRKGTSGSIVTILSNKSGSSGYTLTL 423

QY 444 SGAGYTAGOOLTEVIGCTTVTVSGDGNVPVPMAGGLPRVLVYPTTEKLAGSKICSS 498

Db 424 SSGSYTSLNSGTYTASSVYVEILTCTAVTVDLSNGLAVPMGSLPRVFPESQVLGSGI 621

RESULT 10

JC4510

pullulanase (EC 3.2.1.41) precursor - yeast (lipomyces kononenkoae)

N:Alternate names: LKAL protein; raw starch-degrading amylase

N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)

C:Species: Lipomyces kononenkoae

C:Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004

C:Accession: JC4510; PC4116

R:Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.

Gene 166, 65-71, 1995

A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a lip

A:Reference number: JC4510; MUID:96105202; PMID:8529895

A:Accession: JC4510

A:Molecule type: mRNA

A:Residues: 1-624 <STB>

A:Cross-References: UNIPROT:Q01117; GB:U030376; NID:g1173536; PIDN:AAC49622.1; PID:g11735

A:Experimental source: strain IGC4052B

A:Accession: PC4116

A:Molecule type: protein

A:Residues: 29-44 <ST2>

A:Experimental source: IGC4052B

C:Genetics:

A:Gene: LKAL

C:Function:

A:Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages

A:Pathway: glycogen/starch degradation

C:Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch

C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-624/Product: alpha-amylase #status predicted <MAT>

F:48-141/Domain: glucoamylase starch-binding domain homology <SBD>

F:320-447/Domain: alpha-amylase core homology <AMY>

F:177-185,297-311,387-430,587-622/Disulfide bonds: #status predicted

F:304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 60.7%; Score 1629; DB 1; Length 624;

Best Local Similarity 60.6%; Pred. No. 5e-109;

Matches 292; Conservative 77; Mismatches 113; Indels 0; Gaps 0;

QY 15 AAPALAAPADWRSSQISVFLTLDRFARTDGSSTATCNTADQKCGGTWGIIDKLDYIQG 74

Db 142 SASVPTGTAAWNRGSIYQVVTDRPARTDGSITYSCDVTDVYCGSVYRGIINMLDYIQG 201

QY 75 MGFTAIWLTPTVAQLPOTTAAYGDVHYGWQODIYSLNENYGTADDLKALSSALHERGMYL 134

Db 202 MGFTAIWLTSPVENIPDDTGYGYAHGYWMDKIFALNTNFGADDLIALATELHNRGMYL 261

QY 135 MYDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLP 194

Db 262 MVDIVNHFAPSGNHADVSEYFFYPSSQDYFHSFCWITDYSNQTNVEECWLGDSDVPLV 321

QY 195 LDDTTKDVVKNEWDVWGLSVSNYSIDGLRIDTVKHQKDFPFGYKNAAGVYICGEVIDG 254

Db 322 DVNTQLDVTKSEYQSWVKQLIANYSIDGLRIDTVKHQVQDFWAPQFAAGIYTVGEVFDG 381

QY 255 DPAYTCPTQNVMDGVNLNPIYPIPLINAFKSTSGSMDLYNNMTVKSDCPDSTLLGTTFVE 314

Db 382 DPSYTCPTQENLDGVNLNPPVYVVSAPQFVGSSISLVDMDITLKSECIDTTLTLLGSFLE 441

QY 315 NHDNPRFASVYTNIDIALAKNVAAFIILNDGIPPIIYAGQOHYAGGNDPANREATWLSGYPT 374

Db 442 NQDNPRFYSYSDSLIKNAITLSDGIPPIIYQGEQCLNGNDPYNREALWPTGYST 501

QY 375 DSELYKLIASANAIYNAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGA 434

Db 502 TSTFVEYIASLNQIRNAIYIDDTVLTQNVWVYSDSTIAMRKGTGFTGNQIITVLSNLGS 561

QY 435 SCDSYTSLSGAGYTAGOOLTEVIGCTTVTVSGDGNVPVPMAGGLPRVLVYPTTEKLAGSKI 494

Db 562 SSGSYTSLNSGTYTASSVYVEILTCTAVTVDLSNGLAVPMGSLPRVFPESQVLGSGI 621

QY 495 CS 496

Db 622 CS 623

RESULT 11

S33921

alpha-amylase (EC 3.2.1.1) SWA2 precursor - yeast (Schwanniomyces occidentalis)

N:Alternate names: alpha-1,4 glucanohydrolase

C:Species: Schwanniomyces occidentalis

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: S33921

R:Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.

Curr. Genet. 24, 75-83, 1993

A:Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase fro

A:Reference number: S33921; MUID:93365041; PMID:8358835

A:Accession: S33921

A:Molecule type: DNA

A:Residues: 1-507 <CLA>

A:Cross-References: UNIPROT:Q08806; EMBL:X73497; NID:g3396561; PIDN:CAA51912.1; PID:g33965

C:Genetics:

A:Gene: SWA2

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-507/Product: alpha-amylase #status predicted <MAT>

F:205-332/Domain: alpha-amylase core homology <AMY>

F:134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 1527; DB 2; Length 507;

Best Local Similarity 57.7%; Pred. No. 7.8e-102;

Matches 286; Conservative 74; Mismatches 130; Indels 6; Gaps 3;

QY 1 MVAMSLFLYGLQVAAPALAAPADWRSSQISVFLTLDRFARTDGSSTATCNTADQKCGG 60

Db 17 LVASKPIFLSKRDAGSSAAAA---WRSESIYQLVTDFAFRTDGSSTATCNTGDRVYCGG 72

QY 61 TWQGIIDKLDYIQGFTAIWITPTVAQLPOTTAAYGDVHYGWQODIYSLNENYGTADDL 120

Db 73 TFOGIIDKLDYIQGFTAIWISPVVEIQIPDGTGYAYHYGYWMDKIVAINSNFGTADDL 132

QY 121 KALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180

Db 133 KNLSELHKNRKLMDVIDVTNHYANWGAGSSVAISNYPNPFQOQSYFHDYCLITNTDDQTN 192

QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWDVWGLSVSNYSIDGLRIDTVKHQKDFPFGYK 240

Db 193 VEDCWEGDNTVSLPDLRTEDSDVSSIIFNLVWAEALVSNYSIDGLRIDSAKHVDESFPSPQ 252

QY 241 KAAGVYICGEVIDGDPATCTCPYQNVMDGVNLNPIYPIPLINAFKSTSGSMDLYNNMTVK 300

Db 253 SAAGYLLAGEYVDGDPAYTCPTQNVWGLSVSNYSIDGLRIDTVKHQKDFPFGYKNAAGVYICGEVIDG 312

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:24:00 ; Search time 267.266 Seconds
(without alignments)
954.162 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 2684
Sequence: 1 MYAWSFLYGLQVAAPALA.....LPRVLYPTKLAGSKICSSS 498

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03: *
1: uniprot_prot: *
2: uniprot_tmbl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	2684	100.0	498	2 Q76CT3	Q76ct3 aspergillus
2	2684	100.0	499	1 AMYA_ASPOR	P10529 aspergillus
3	2680	99.9	499	2 Q76L59	Q76l59 aspergillus
4	2675	99.7	499	1 AMY_ASPSH	P30292 aspergillus
5	2674	99.6	499	1 AMYB_ASPAW	Q02906 aspergillus
6	2674	99.6	499	2 Q96TH4	Q96th4 aspergillus
7	2674	99.6	499	2 Q7LV45	Q7lv45 aspergillus
8	2662	99.2	498	1 AMYA_ASPAW	Q02905 aspergillus
9	1826	68.0	490	2 Q9UV07	Q9uv07 emericella
10	1810	67.4	640	2 O13296	O13296 aspergillus
11	1791	66.7	634	2 Q76L96	Q76l96 aspergillus
12	1778	66.2	484	1 AMYA_ASPNG	P56271 aspergillus
13	1725.5	64.3	623	2 Q9UV09	Q9uv09 emericella
14	1662	61.9	647	2 Q6YF33	Q6yf33 lipomyces s
15	1629	60.7	624	1 AMY1_LIPKO	Q01117 lipomyces k
16	1527	56.9	507	1 AMY2_DBOC	Q08806 debaryomyce
17	1449	54.0	512	1 AMY1_DBOC	P19267 debaryomyce
18	1397.5	52.1	494	1 AMY1_SACFI	P21567 saccharomyc
19	1272.5	47.4	492	2 Q7SDJ6	Q7sdj6 neurospora
20	1264	47.1	631	2 Q92394	Q92394 cryptococcu
21	1056.5	39.4	533	2 Q784K0	Q784k0 neurospora
22	1015.5	37.8	513	1 AMY3_SCHPO	O14154 schizosacch
23	963.5	35.9	625	2 Q74922	Q74922 schizosacch
24	920.5	34.3	491	2 O13996	O13996 schizosacch
25	899	33.5	581	1 AMY1_SCHPO	Q09840 schizosacch
26	898.5	33.5	564	1 AMY4_SCHPO	Q9y789 schizosacch
27	898	33.5	478	1 YQ29_SCHPO	Q10427 schizosacch
28	895	33.3	499	2 Q8JLE4	Q8jle4 lipomyces k
29	737	27.5	482	2 Q60051	Q60051 thermoactin
30	670	25.0	1196	1 AMYB_PAEPO	P21543 paenibacill
31	653.5	24.3	774	1 AMY2_SCHPO	O42318 schizosacch

32 481.5 17.9 642 2 Q8Z0C9
33 479.5 17.9 642 2 Q8RMG0
34 461.5 17.2 877 2 Q87FT5
35 456.5 17.0 713 1 CDGT_BACSO
36 454.5 16.9 712 1 CDGT_BACS3
37 453 16.9 1798 2 Q9KZ11
38 450 16.8 719 1 AMYM_BACST
39 447.5 16.7 712 2 Q6S3E3
40 447.5 16.7 713 2 Q9F5W3
41 444.5 16.6 713 1 CDGT_BAC11
42 440.5 16.4 528 2 AMY_BACCI
43 436 16.2 1806 2 Q82AS4
44 433 16.1 710 1 CDGT_THETU
45 430.5 16.0 524 2 Q8R900

ALIGNMENTS

RESULT 1

Q76CT3 ID Q76CT3 PRELIMINARY; PRT; 498 AA.
AC Q76CT3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase.
DE Name=amyA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito K.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB109452; EAD01051.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;

Query Match 100.0%; Score 2684; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 2e-178;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAWSFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCYCG 60
DB 1 MYAWSFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCYCG 60
QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDAHYGWQQDIYSLNENYGTADDL 120
DB 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDAHYGWQQDIYSLNENYGTADDL 120
QY 121 KALSALHGERGMVMDVVDVNVANHMGVDGAGSSVDYSVFKPFPSSQDYHPFCFIQNYEDQIQ 180
DB 121 KALSALHGERGMVMDVVDVNVANHMGVDGAGSSVDYSVFKPFPSSQDYHPFCFIQNYEDQIQ 180
QY 181 VEDCWLGDNTVSLPDLDTTKDVVQNEWYDWVGLSVNSYISIDGLRIDTVKHVKQDFWPGYN 240
DB 181 VEDCWLGDNTVSLPDLDTTKDVVQNEWYDWVGLSVNSYISIDGLRIDTVKHVKQDFWPGYN 240
QY 241 KAAGVYICIGVLDDGPAYTCPYQNVMDGVNLPIYYPLLNAPFKSTSGSMDLLYNNMINTVK 300
DB 241 KAAGVYICIGVLDDGPAYTCPYQNVMDGVNLPIYYPLLNAPFKSTSGSMDLLYNNMINTVK 300
QY 301 SDCPSTLLGTTFVHNDRPFASYTNDIALAKNVAAPFIINDGIPPIYAQEQEHYAGND 360

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Db 301 SDCPDSTLLGTFVFNHNDNPRFASYNIDIALKNVAAFIILNDGIPITVYAGQBOHYAGND 360
Qy 361 PANREATWISGVPTDSSELYKLASANAIAENVAISKDTGVTYKNWPIYKDDTTIAMRKCT 420
Db 361 PANREATWISGVPTDSSELYKLASANAIAENVAISKDTGVTYKNWPIYKDDTTIAMRKCT 420
Qy 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVGSDGNVVPVAGGLP 480
Db 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVGSDGNVVPVAGGLP 480
Qy 481 RVLYPTEKLAGSKICSSS 498
Db 481 RVLYPTEKLAGSKICSSS 498

RESULT 2
AMTA ASPOR
ID ID AMYA ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-D-glucanase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
GN Name=AMY1;
GN and
GN Name=AMY2;
GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RX MEDLINE=89237897; PubMed=2785629;
RA Wiesel S., Lachmund A., Wildhardt G., Rutkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RT Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Taikagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Uda S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";
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RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.
CC -!- SUBUNIT: Monomer.
CC -!- BIOTECHNOLOGY: Used in the brewing industry to increase the
CC fermentability of beer worts (including those made from unmalted
CC cereals), in the starch industry to make high maltose and high DE
CC syrups (starch saccharification), in the alcohol industry to
CC reduce fermentation time, in the cereal food industry for flour
CC supplementation and improvement of chilled and frozen dough, and
CC in the forestry industry for low-temperature modification of
CC starch. Sold under the name Fungamyl by Novozymes.
CC -!- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X12725; CAA31218.1; -
CC EMBL; X12726; CAA31219.1; -
CC EMBL; X12727; CAA31220.1; -
CC EMBL; D00434; BAA00336.1; -
CC EMBL; M33218; AAA32708.1; -
CC PIR; JTK0201; JTK0201.
CC PIR; JTK0456; JTK0466.
CC PIR; S04548; ALAS1.
CC PDB; 2TAA; X-ray; A=22-499.
CC PDB; 6TAA; X-ray; @=22-499.
CC PDB; 7TAA; X-ray; @=22-499.
CC GlycoSuiteDB; P10529; -
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC 3D-structure; Calcium-binding; Carbohydrate metabolism;
KW Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
KW Multigene family; Signal.
FT SIGNAL 1 29
FT CHAIN 22 499 Alpha-amylase A.
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227	227	ACT_SITE	Nucleophile.	Query Match	100.0%;	Score 2684;	DB 1;	Length 499;
251	251	ACT_SITE	Proton donor.	Best Local Similarity	100.0%;	Pred. No. 2e-178;		
318	318	ACT_SITE		Matches	498;	Conservative	0;	Mismatches
142	142	METAL					0;	Indels
183	183	METAL	Calcium 1.					
196	196	METAL	Calcium 1 (via carbonyl oxygen).					
227	227	METAL	Calcium 1.					
231	231	METAL	Calcium 2.					
251	251	METAL	Calcium 2.					
51	51	DISULFID						
171	171	DISULFID						
304	304	DISULFID						
461	461	DISULFID						
218	218	CARBOHYD						
56	56	VARIANT	N-linked (GlcNAc. . .).					
172	172	VARIANT	/FTIG=CAR_000125.					
93	93	CONFLICT	Q -> R (in AMY3).					
106	106	CONFLICT	F -> L (in AMY3).					
184	184	CONFLICT	TT -> DC (in Ref. 5).					
195	195	CONFLICT	Q -> T (in Ref. 5).					
255	255	CONFLICT	D -> Y (in Ref. 3).					
291	291	CONFLICT	P -> L (in Ref. 3).					
345	345	CONFLICT	G -> V (in Ref. 3).					
370	370	CONFLICT	D -> H (in Ref. 4).					
406	406	CONFLICT	I -> L (in Ref. 5).					
448	448	CONFLICT	L -> A (in Ref. 4).					
497	497	CONFLICT	WPIY -> PYI (in Ref. 5).					
24	24	HELIX	G -> S (in Ref. 5).					
28	28	TURN	S -> SD (in Ref. 5 and 7).					
32	32	STRAND						
37	37	HELIX						
42	42	TURN						
43	43	TURN						
53	53	HELIX						
61	61	STRAND						
63	63	HELIX						
69	69	TURN						
70	70	HELIX						
75	75	TURN						
80	80	STRAND						
83	83	STRAND						
87	87	STRAND						
94	94	STRAND						
95	95	TURN						
97	97	TURN						
100	100	TURN						
105	105	STRAND						
113	113	TURN						
118	118	HELIX						
131	131	TURN						
134	134	STRAND						
143	143	STRAND						
146	146	STRAND						
150	150	HELIX						
155	155	HELIX						
159	159	STRAND						
164	164	HELIX						
167	167	STRAND						
172	172	STRAND						
176	176	TURN						
184	184	HELIX						
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196	196	STRAND						
199	199	TURN						
202	202	HELIX						
220	220	TURN						
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244	244	TURN						
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251	251	ACT_SITE	Proton donor.	Best Local Similarity	100.0%;	Pred. No. 2e-178;		
318	318	ACT_SITE		Matches	498;	Conservative	0;	Mismatches
142	142	METAL					0;	Indels
183	183	METAL	Calcium 1.					
196	196	METAL	Calcium 1 (via carbonyl oxygen).					
227	227	METAL	Calcium 1.					
231	231	METAL	Calcium 2.					
251	251	METAL	Calcium 2.					
51	51	DISULFID						
171	171	DISULFID						
304	304	DISULFID						
461	461	DISULFID						
218	218	CARBOHYD						
56	56	VARIANT	N-linked (GlcNAc. . .).					
172	172	VARIANT	/FTIG=CAR_000125.					
93	93	CONFLICT	Q -> R (in AMY3).					
106	106	CONFLICT	F -> L (in AMY3).					
184	184	CONFLICT	TT -> DC (in Ref. 5).					
195	195	CONFLICT	Q -> T (in Ref. 5).					
255	255	CONFLICT	D -> Y (in Ref. 3).					
291	291	CONFLICT	P -> L (in Ref. 3).					
345	345	CONFLICT	G -> V (in Ref. 3).					
370	370	CONFLICT	D -> H (in Ref. 4).					
406	406	CONFLICT	I -> L (in Ref. 5).					
448	448	CONFLICT	L -> A (in Ref. 4).					
497	497	CONFLICT	WPIY -> PYI (in Ref. 5).					
24	24	HELIX	G -> S (in Ref. 5).					
28	28	TURN	S -> SD (in Ref. 5 and 7).					
32	32	STRAND						
37	37	HELIX						
42	42	TURN						
43	43	TURN						
53	53	HELIX						
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63	63	HELIX						
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70	70	HELIX						
75	75	TURN						
80	80	STRAND						
83	83	STRAND						
87	87	STRAND						
94	94	STRAND						
95	95	TURN						
97	97	TURN						
100	100	TURN						
105	105	STRAND						
113	113	TURN						
118	118	HELIX						
131	131	TURN						
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143	143	STRAND						
146	146	STRAND						
150	150	HELIX						
155	155	HELIX						
159	159	STRAND						
164	164	HELIX						
167	167	STRAND						
172	172	STRAND						
176	176	TURN						
184	184	HELIX						
186	186	STRAND						
196	196	STRAND						
199	199	TURN						
202	202	HELIX						
220	220	TURN						
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229	229	HELIX						
234	234	TURN						
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244	244	TURN						
245	245	TURN						
227	227	ACT_SITE	Nucleophile.	Query Match	100.0%;	Score 2684;	DB 1;	Length 499;
251	251	ACT_SITE	Proton donor.	Best Local Similarity	100.0%;	Pred. No. 2e-178;		
318	318	ACT_SITE		Matches	498;	Conservative	0;	Mismatches
142	142	METAL					0;	Indels
183	183	METAL	Calcium 1.					
196	196	METAL	Calcium 1 (via carbonyl oxygen).					
227	227	METAL	Calcium 1.					
231	231	METAL	Calcium 2.					
251	251	METAL	Calcium 2.					
51	51	DISULFID						
171	171	DISULFID						
304	304	DISULFID						
461	461	DISULFID						
218	218	CARBOHYD						
56	56	VARIANT	N-linked (GlcNAc. . .).					
172	172	VARIANT	/FTIG=CAR_000125.					
93	93	CONFLICT	Q -> R (in AMY3).					
106	106	CONFLICT	F -> L (in AMY3).					
184	184	CONFLICT	TT -> DC (in Ref. 5).					
195	195	CONFLICT	Q -> T (in Ref. 5).					
255	255	CONFLICT	D -> Y (in Ref. 3).					
291	291	CONFLICT	P -> L (in Ref. 3).					
345	345	CONFLICT	G -> V (in Ref. 3).					
370	370	CONFLICT	D -> H (in Ref. 4).					
406	406	CONFLICT	I -> L (in Ref. 5).					
448	448	CONFLICT	L -> A (in Ref. 4).					
497	497	CONFLICT	WPIY -> PYI (in Ref. 5).					
24	24	HELIX	G -> S (in Ref. 5).					
28	28	TURN	S -> SD (in Ref. 5 and 7).					
32	32	STRAND						
37	37	HELIX						
42	42	TURN						
43	43	TURN						
53	53	HELIX						
61	61	STRAND						
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69	69	TURN						
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118	118	HELIX						
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146	146	STRAND						
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155	155	HELIX						
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167	167	STRAND						
172	172	STRAND						
176	176	TURN						
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199	199	TURN						
202	202	HELIX						
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223	223	STRAND						
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244	244	TURN						
245	245	TURN						
227	227	ACT_SITE	Nucleophile.	Query Match	100.0%;	Score 2684;	DB 1;	Length 499;
251	251	ACT_SITE	Proton donor.	Best Local Similarity	100.0%;	Pred. No. 2e-178;		
318	318	ACT_SITE		Matches	498;	Conservative	0;	Mismatches
142	142	METAL					0;	Indels
183	183	METAL	Calcium 1.					
196	196	METAL	Calcium 1 (via carbonyl oxygen).					
227	227	METAL	Calcium 1.					
231	231	METAL	Calcium 2.					
251	251	METAL	Calcium 2.					
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171	171</							

Query Match 99.9%; Score 2680; DB 2; Length 499;
 Best Local Similarity 99.8%; Pred. No. 3.9e-178;
 Matches 497; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSOSIYFLLTDRPARTDGGTTATCNTADQKCGG 60
 DB 2 MVAMWSFLYGLQVAAPALAAPADWRSOSIYFLLTDRPARTDGGTTATCNTADQKCGG 61
 QY 61 TWQGIIDKLDYIQGSGFTAIWITPTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 120
 DB 62 TWQGIIDKLDYIQGSGFTAIWITPTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 121
 QY 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
 DB 122 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 181
 QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240
 DB 182 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 241
 QY 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVNLNPIYPLNNAFKSTSGSMDLLYNNINTVK 300
 DB 242 KAAGYVCIGEVLDGDPAYTCYQNVMDGVNLNPIYPLNNAFKSTSGSMDLLYNNINTVK 301
 QY 301 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIIPIIYAGQBOHYAGND 360
 DB 302 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIIPIIYAGQBOHYAGND 361
 QY 361 PANREATWLSGYPTDSELYKLIASANAIKSDTGFVTYKKNWPIYKDDTTIAMRGT 420
 DB 362 PANREATWLSGYPTDSELYKLIASANAIKSDTGFVTYKKNWPIYKDDTTIAMRGT 421
 QY 421 DGSQIVTILSNKAGSDSYTILSLGAGYTAGOQLTEVIGCTTTVVGSDGNVPPVPMAGGLP 480
 DB 422 DGSQIVTILSNKAGSDSYTILSLGAGYTAGOQLTEVIGCTTTVVGSDGNVPPVPMAGGLP 481
 QY 481 RVLVPTKLAGSKICSSS 498
 DB 482 RVLVPTKLAGSKICSSS 499

RESULT 4
 ID AMY ASPSH
 AC P30292; STANDARD; PRT; 499 AA.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN Name=AMY;
 OS Aspergillus shirousami.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Euryotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5070;
 RN [1]_____
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92323146; PubMed=1368777;
 RA Shibuya I., Tamura G., Ishikawa T., Hara S.;
 RT "Cloning of the alpha-amylase cDNA of Aspergillus shirousami and its
 RT expression in Saccharomyces cerevisiae."
 RL Bionci. Biotechnol. Biochem. 56:174-179(1992).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC
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 CC -----

DR EMBL; D10461; BAA01255.1; -.
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF0128; Alpha-amy1ase; 1.
 DR PRINTS; PRO0110; ALPHAAMYLASE.
 DR SMART; SM00642; Aamy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 499
 FT ACT_SITE 227 227
 FT ACT_SITE 251 251
 FT ACT_SITE 318 318
 FT METAL 142 142
 FT METAL 183 183
 FT METAL 196 196
 FT METAL 227 227
 FT METAL 231 231
 FT METAL 251 251
 FT DISULFID 51 59
 FT DISULFID 171 185
 FT DISULFID 261 304
 FT DISULFID 461 496
 FT CARBOHYD 218 218
 SQ SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;

Alpha-amy1ase.
 Nucleophile (By similarity).
 Proton donor (By similarity).
 By similarity.
 Calcium 1 (By similarity).
 Calcium 1 (via carbonyl oxygen) (By similarity).
 Calcium 1 (By similarity).
 Calcium 2 (By similarity).
 By similarity.
 By similarity.
 By similarity.
 By similarity.
 N-linked (GlcNAc...) (By similarity).
 1PB7AE50DA01C03F CRC64;

Query Match 99.7%; Score 2675; DB 1; Length 499;
 Best Local Similarity 99.8%; Pred. No. 8.6e-178;
 Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSOSIYFLLTDRPARTDGGTTATCNTADQKCGG 60
 DB 2 MVAMWSFLYGLQVAAPALAAPADWRSOSIYFLLTDRPARTDGGTTATCNTADQKCGG 61
 QY 61 TWQGIIDKLDYIQGSGFTAIWITPTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 120
 DB 62 TWQGIIDKLDYIQGSGFTAIWITPTAQLPQTAYGDVHGYWQDIYSLNENYGTADDL 121
 QY 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
 DB 122 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 181
 QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240
 DB 182 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 241
 QY 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVNLNPIYPLNNAFKSTSGSMDLLYNNINTVK 300
 DB 242 KAAGYVCIGEVLDGDPAYTCYQNVMDGVNLNPIYPLNNAFKSTSGSMDLLYNNINTVK 301
 QY 301 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIIPIIYAGQBOHYAGND 360
 DB 302 SDCPDSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIIPIIYAGQBOHYAGND 361
 QY 361 PANREATWLSGYPTDSELYKLIASANAIKSDTGFVTYKKNWPIYKDDTTIAMRGT 420
 DB 362 PANREATWLSGYPTDSELYKLIASANAIKSDTGFVTYKKNWPIYKDDTTIAMRGT 421
 QY 421 DGSQIVTILSNKAGSDSYTILSLGAGYTAGOQLTEVIGCTTTVVGSDGNVPPVPMAGGLP 480
 DB 422 DGSQIVTILSNKAGSDSYTILSLGAGYTAGOQLTEVIGCTTTVVGSDGNVPPVPMAGGLP 481
 QY 481 RVLVPTKLAGSKICSSS 498
 DB 482 RVLVPTKLAGSKICSSS 499


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RESULT 5
ID AMYB ASPAW STANDARD; PRT; 499 AA.
AC Q02906;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase B).
GN Name=AMYB;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DVK143F;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC -----
DR EMBL; X52756; CAA36967.1; -.
DR PIR; B48305; B48305.
DR HSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 499 Alpha-amylase B.
FT ACT_SITE 227 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).
FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 499 AA; 54921 MW; 740B96B11BC01A8A CRC64;
Query Match 99.6%; Score 2674; DB 1; Length 499;
Best Local Similarity 99.6%; Pred. No. 1e-177; 2; Indels 0; Gaps 0;
Matches 496; Conservative 0; Mismatches 2;

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RESULT 6

Q96TH4

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ID Q96TH4 PRELIMINARY; PRT; 499 AA.
AC Q96TH4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Taka-amylase A (EC 3.2.1.1).
GN Name=amyA;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RIB40;
RX MEDLINE=20289310; PubMed=10830498;
RA Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
RT gene, amyR, involved in the amylolytic gene expression in Aspergillus
RT oryzae.";
RL Biosci. Biotechnol. Biochem. 64:816-827(2000).
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB021876; BAA95703.1; -.
DR PIR; JN0588; JN0588.
DR PIR; S04549; ALA83.
DR HSP; P10529; 7TAA.
DR CO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.

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DR SMART; SM00642; Amy; 1.
DR Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match          99.6%; Score 2674; DB 2; Length 499;
Best Local Similarity 99.6%; Pred. No. 1e-177;
Matches 496; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTATCNTADOKYCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTATCNTADOKYCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVHGYWQODIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVHGYWQODIYSLNENYGTADDL 121
QY 121 KALSSALHERGMVLMVDVVAHMGVDGAGSSVDYVFPPSSQDYFHPFCFIONYEDQTO 180
DB 122 KALSSALHERGMVLMVDVVAHMGVDGAGSSVDYVFPPSSQDYFHPFCFIONYEDQTO 181
QY 181 VEDCWLGNTVSLPDLDTTKOVVKNNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
DB 182 VEDCWLGNTVSLPDLDTTKOVVKNNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 241
QY 241 KAAGYVCIGEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAPFKSTSGMDDLNNMINTVK 300
DB 242 KAAGYVCIGEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAPFKSTSGMDDLNNMINTVK 301
QY 301 SDCPSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGND 360
DB 302 SDCPSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKT 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKT 421
QY 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLP 481
QY 481 RVLVYTEKLAGSKICSSS 498
DB 482 RVLVYTEKLAGSKICSSS 499

RESULT 7
Q7LV45 PRELIMINARY; PRT; 499 AA.
AC Q7LV45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Alpha-amylase (EC 3.2.1.1).
GN Name=amy1;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5059;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-10D;
RA Fakhoury A.M., Weloshek C.P.;
RT "Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in
RT aflatoxin biosynthesis in maize kernels.";
RL Phytopathology 89:908-914 (1999).
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF139925; AAF14264.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match          99.6%; Score 2674; DB 2; Length 499;
Best Local Similarity 99.6%; Pred. No. 1e-177;
Matches 496; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTATCNTADOKYCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTATCNTADOKYCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVHGYWQODIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVHGYWQODIYSLNENYGTADDL 121
QY 121 KALSSALHERGMVLMVDVVAHMGVDGAGSSVDYVFPPSSQDYFHPFCFIONYEDQTO 180
DB 122 KALSSALHERGMVLMVDVVAHMGVDGAGSSVDYVFPPSSQDYFHPFCFIONYEDQTO 181
QY 181 VEDCWLGNTVSLPDLDTTKOVVKNNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
DB 182 VEDCWLGNTVSLPDLDTTKOVVKNNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 241
QY 241 KAAGYVCIGEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAPFKSTSGMDDLNNMINTVK 300
DB 242 KAAGYVCIGEVLGDGPAYTCPYQNVMDGVNLNPIYYPILLNAPFKSTSGMDDLNNMINTVK 301
QY 301 SDCPSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGND 360
DB 302 SDCPSTLLGTFFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKT 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKT 421
QY 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTSGDGNVPPVPMAGGLP 481
QY 481 RVLVYTEKLAGSKICSSS 498
DB 482 RVLVYTEKLAGSKICSSS 499

RESULT 8
AMYA ASPAW STANDARD; PRT; 498 AA.
AC Q02905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase A).
GN Name=AMYA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212 (1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
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CC at high concentrations (By similarity).
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; X52755; CAA36966.1; -;
 CC PIR; A48305; A48305.
 CC HSP; P10529; 7TAA.
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; Alpha-amy1ase; 1.
 CC PRINTS; PR00110; ALPHAAMYLASE.
 CC SMART; SM00642; Amy; 1.
 CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Multigene family; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 498 Alpha-amy1ase A.
 FT ACT_SITE 227 227 Nucleophile (By similarity).
 FT ACT_SITE 251 251 Proton donor (By similarity).
 FT ACT_SITE 318 318 By similarity.
 FT METAL 142 142 Calcium 1 (By similarity).
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 498 AA; 54880 MW; 7658511BC01A8A01 CRC64;
 Query Match 99.2%; Score 2662; DB 1; Length 498;
 Best Local Similarity 99.6%; Pred. No. 6.9e-177;
 Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MVAWNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 60
 DB 2 MVAWNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 61
 QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDAYHYGQQDIYSLNENYGTADDL 120
 DB 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDAYHYGQQDIYSLNENYGTADDL 121
 QY 121 KALSSALHGRMYLVVDVNVANMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTO 180
 DB 122 KALSSALHGRMYLVVDVNVANMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTO 181
 QY 181 VEDCWLGDNTVSLPDLDTTKDVVKVNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240
 DB 182 VEDCWLGDNTVSLPDLDTTKDVVKVNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 241
 QY 241 KAAGVYICIGELVDGDPAYTCYQNVMDGVNLPIYYPYLLNAFKSTSGSMDLLYNNMINTVK 300
 DB 242 KAAGVYICIGELVDGDPAYTCYQNVMDGVNLPIYYPYLLNAFKSTSGSMDLLYNNMINTVK 301
 QY 301 SCQPDSTLLGTFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGQSHYAGGND 360
 DB 302 SCQPDSTLLGTFVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGQSHYAGGND 361
 QY 361 PANREATWLSGYPDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKCT 420
 DB 362 PANREATWLSGYPDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKCT 421

QY 421 DGSQIVTILSNKAGSDSYTILSGAGYTAGOOLTEVICCTTTVTCSDGNVPVPMAGGLP 480
 DB 422 DGSQIVTILSNKAGSDSYTILSGAGYTAGOOLTEVICCTTTVTCSDGNVPVPMAGGLP 481
 QY 481 RVLYPTEKLAGSKIC 495
 DB 482 RVLYPTEKLAGSKIC 496
 RESULT 9
 QYUV07
 ID QYUV07 PRELIMINARY; PRT; 490 AA.
 AC QYUV07;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Alpha-amy1ase AmyA.
 GN Name=amyA;
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boase N.A., Murphy R.M., Kelly J.M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 DR EMBL; AF208225; AAF17103.1; -;
 DR HSP; P10529; 7TAA.
 DR GO; GO:0004556; F:alpha-amy1ase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amy1ase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 490 AA; 54249 MW; A891C4ACEABE5305 CRC64;
 Query Match 68.0%; Score 1826; DB 2; Length 490;
 Best Local Similarity 69.6%; Pred. No. 1e-118;
 Matches 337; Conservative 53; Mismatches 92; Indels 2; Gaps 2;
 QY 12 LQVAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDY 71
 DB 7 LQVAPALAAPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDY 65
 QY 72 IQGMGFTAIWTPVTAQLPQTAYGDAYHYGQQDIYSLNENYGTADDL KALSSALHGR 131
 DB 66 IQGMGFTAIWTPVTAQLPQTAYGDAYHYGQQDIYSLNENYGTADDL KALSSALHGR 124
 QY 132 MYLVVDVNVANMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTOVEDCWLGDNTV 191
 DB 125 MYLVVDVNVANMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTOVEDCWLGDNTV 184
 QY 192 SLDPDLDTTKDVVKVNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEV 251
 DB 185 SLDPDLDTTKDVVKVNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEV 244
 QY 252 LQGDGPAYTCYQNVMDGVNLPIYYPYLLNAFKSTSGSMDLLYNNMINTVKSDCPDSTLLGCT 311
 DB 245 LQGDGPAYTCYQNVMDGVNLPIYYPYLLNAFKSTSGSMDLLYNNMINTVKSDCPDSTLLGCT 304
 QY 312 FVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGQSHYAGGNDPANREATWLSG 371
 DB 305 FVENHNDNPRFASYTNDIALAKNVAAPFIILNDGIPPIYAGQSHYAGGNDPANREATWLSG 364
 QY 372 YPTDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKCTGSGQIVTILSN 431
 DB 365 YPTDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKCTGSGQIVTILSN 424
 QY 432 KASGSDSYTILSNKAGSDSYTILSGAGYTAGOOLTEVICCTTTVTCSDGNVPVPMAGGLP 491

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Db 425 AGADAGSSTVSVPNTGFTAGAAVTEIYTCEDITVSGSGEVSPMESGLPRVLYPRAKLEG 484
QY 492 SKIC 495
Db 485 SGIC 488

RESULT 10
O13296
ID O13296 PRELIMINARY; PRT; 640 AA.
AC O13296;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Acid-stable alpha-amylose.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko A., Sudo S., Sakamoto Y., Tamura G., Ishikawa T., Ohba T.;
RT "Molecular-cloning and determination of the nucleotide-sequence of a
RT gene encoding an acid-stable alpha-amylose from Aspergillus-
RT kawachi.";
RL J. Ferment. Bioeng. 81:292-298(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Kaneko A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008370; BAA22993.1; -.
DR HSP; P56271; 2AAA.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylose; 1.
DR Pfam; PF06886; CBM_20; 1.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 640 AA; 69507 MW; 676BF9D0236720DD CRC64;

Query Match 67.4%; Score 1810; DB 2; Length 640;
Best Local Similarity 67.6%; Pred. No. 1.9e-117;
Matches 325; Conservative 66; Mismatches 90; Indels 0; Gaps 0;

QY 18 ALAATPADWRSSQSIYFLLTDRFARTDGTATCNTADQKCYCGTWQGIIDKLDYIQGMGF 77
Db 19 ALGLSAAEWRTQSIYFLLTDRFRTDNTTATCNTGDQIYCGSGWQGIINHLDIYQGMGF 78
QY 78 TAIWTPVTAQLPQTAYGDVHYGWQDIYSLNENYGTADDLKSALHRCMYLMD 137
Db 79 TAIWISPIEQLPQDTSDEAYHGYWQKIYVYNSNFGTADDLKSALHARGMYLMD 138
QY 138 VVANHMGVDGAGSSVDYSVFPFSSQDYFHPFCFTQNTVEDQVDEDCWLGNTVSLPDL 197
Db 139 VVPNHMGVAGNGNDVYSVFPDFSSSYFHPYCLITDNDLTMWQDCWEGDTIVSLPDLN 198
QY 198 TTKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGYVCIGEVLDGPA 257
Db 199 TTETAVRIWDVADLVSNYSVDGLRIDSVEEVEPDPFPQYQEAAGYVCIGEVLDGPA 258
QY 258 YTCPVQNVMDGVNLYPIYPLINAFKSTSGMDDLNNMINTVKSDDCPDSTLLGTFFVENHD 317
Db 259 LDCPYQKLDGVNLYPIYQLLYAFESSSGSISNLYNMKSVASDCSDPTLLGNFIENHD 318
QY 318 NPFASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSE 377
Db 319 NPFASYTSDYSQAKNVLISFLSGIPIVYAGEEHYSGGDPVYNREATWLSGYDTSAE 378
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QY 378 LYKLIASANAI RNVAISKDTGFTVYKWPYIKDDTTIAMRKGTGDSQIVTILSNKGASGD 437
Db 379 LYTWIATTNAIKLAISADSDYIYKNDPIYDTSNTIAMRKGTSGSIIIVLSNKGSSGS 438
QY 438 SYTSLSGAGYTAGOOLTEVIGCTTGVGSDGNVPMAGGLPRVLYPTEKLAGSKICSS 497
Db 439 SYTLTLGSGYTSGLTKLIEAVTCTSVTVDSNGDIPVPMASGLPVLPLASVVVDSLSLCCG 498
QY 498 S 498
Db 499 S 499

RESULT 11
O76L96
ID O76L96 PRELIMINARY; PRT; 634 AA.
AC O76L96;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Alpha-amylose precursor.
GN Name=amyl III;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083162; BAD06005.1; -.
DR EMBL; AB083160; BAD06003.1; -.
DR HSP; P04064; IACZ.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylose; 1.
DR Pfam; PF06886; CBM_20; 1.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Aamy; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 634 AA; 69242 MW; 16C0BB6AF6FB0E9B CRC64;

Query Match 66.7%; Score 1791; DB 2; Length 634;
Best Local Similarity 68.6%; Pred. No. 3.9e-116;
Matches 321; Conservative 64; Mismatches 83; Indels 0; Gaps 0;

QY 18 ALAATPADWRSSQSIYFLLTDRFARTDGTATCNTADQKCYCGTWQGIIDKLDYIQGMGF 77
Db 19 ALGLSAAEWRTQSIYFLLTDRFRTDNTTATCNTGDQIYCGSGWQGIINHLDIYQGMGF 78
QY 78 TAIWTPVTAQLPQTAYGDVHYGWQDIYSLNENYGTADDLKSALHRCMYLMD 137
Db 79 TAIWISPIEQLPQDTSDEAYHGYWQKIYVYNSNFGTADDLKSALHARGMYLMD 138
QY 138 VVANHMGVDGAGSSVDYSVFPFSSQDYFHPFCFTQNTVEDQVDEDCWLGNTVSLPDL 197
Db 139 VVPNHMGVAGNGNDVYSVFPDFSSSYFHPYCLITDNDLTMWQDCWEGDTIVSLPDLN 198
QY 198 TTKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGYVCIGEVLDGPA 257
Db 199 TTETAVRIWDVADLVSNYSVDGLRIDSVEEVEPDPFPQYQEAAGYVCIGEVLDGPA 258
QY 258 YTCPVQNVMDGVNLYPIYPLINAFKSTSGMDDLNNMINTVKSDDCPDSTLLGTFFVENHD 317
Db 259 LDCPYQKLDGVNLYPIYQLLYAFESSSGSISNLYNMKSVASDCSDPTLLGNFIENHD 318
QY 318 NPFASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSE 377
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FT	STRAND	73	73
FT	TURN	74	75
FT	STRAND	76	76
FT	TURN	79	80
FT	STRAND	84	90
FT	TURN	92	94
FT	HELIX	97	108
FT	TURN	109	111
FT	STRAND	113	118
FT	STRAND	122	122

FT	HELIX	134	136
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FT	STRAND	138	138	133	6
FT	HELIX	143	143	145	
FT	STRAND	146	146	146	
FT	STRAND	151	151	151	
FT	TURN	155	155	156	
FT	HELIX	158	158	163	
FT	STRAND	165	165	167	
FT	STRAND	172	172	173	
FT	STRAND	175	175	176	
FT	TURN	178	178	179	
FT	HELIX	181	181	198	
FT	TURN	199	199	199	
FT	STRAND	202	202	205	
FT	TURN	209	209	210	
FT	HELIX	213	213	215	
FT	STRAND	216	216	223	
FT	TURN	224	224	224	
FT	STRAND	226	226	229	
FT	HELIX	236	236	239	
FT	HELIX	240	240	244	
FT	TURN	245	245	245	
FT	STRAND	248	248	250	
FT	HELIX	252	252	262	
FT	TURN	265	265	266	
FT	HELIX	269	269	282	
FT	HELIX	286	286	288	
FT	STRAND	290	290	291	
FT	TURN	296	296	297	
FT	HELIX	301	301	303	
FT	TURN	304	304	304	
FT	HELIX	308	308	320	
FT	STRAND	324	324	328	
FT	TURN	329	329	334	
FT	TURN	339	339	343	
FT	HELIX	347	347	350	
FT	TURN	351	351	352	
FT	TURN	354	355	355	
FT	HELIX	357	357	375	
FT	TURN	377	377	381	
FT	STRAND	385	385	390	
FT	TURN	391	391	392	
FT	STRAND	393	398	398	
FT	TURN	401	401	403	
FT	STRAND	405	410	410	
FT	TURN	414	414	415	
FT	STRAND	419	419	423	
FT	TURN	430	430	431	
FT	STRAND	433	436	433	
FT	TURN	437	440	440	
FT	STRAND	441	444	441	
FT	TURN	447	448	447	
FT	STRAND	451	455	455	
FT	TURN	457	458	461	
FT	STRAND	461	465	469	
FT	HELIX	466	466	470	
FT	TURN	470	471	471	
FT	TURN	474	474	475	
SQ	SEQUENCE	484	AA;	52	

Query Match

Best Local Similarity		66.9%	Pred. No. 2.2e-115;	Matches 318; Conservative 63; Mismatches 94; Indels 0; Gaps 0;	
QY	24	ADRSQSIYFLLTDRFARTDGSSTTACNTADOKYCCGTWQGIIDKLVDYIQMGFTAIWIT	83		
Db	4	ASWRTQSIYFLLTDRFRGTDNSTTACNTGNEIYCGSSWQGIIDHLDYIEGNGFTAIWIS	63		
QY	84	PVTAQLPQTATGDAYHYGWOQDIYSLNENYGTADDLKALSSALHARGMYLWMDVVAHNM	143		
Db	64	PITEQLPQDTADGEAYHYGWOQKIYDVSNGPFGTADNLKSLSDALHARGMYLWMDVVPDHM	123		
QY	144	GYDAGSSVDYSVFKPFSSQDYHPPFCFIQNYEDQTOVEDCWLGDNTVSLPDLDTTKDXY	203		
Db	124	GYAGNGNDVDSVFPDPSSSYFPHYCLITDMDNLTWBECWEGDITVSLPDLDTTETAV	183		
QY	204	KNEWYDVGSLVSNYSIDGLRIDITVRKHVQKDFWPGYNKAAAGVYICIGVLQDGPAYTCPYQ	263		
Db	184	RTIYDWADVADLSVNSYVDGLRIDSVLEVPQDFPGYNKASGVYCVGEIDNGNPASDCPYQ	243		
QY	264	NVMDGVNLNPIIYPLLNAPFKSTSGSMDLLNMINTVKSDCPDSTLLGTFFVENHDNPRPAS	323		
Db	244	KVLDEGVNLNPIYMWLLYAFESSGSIISNLNMIKSVASDCSDPTLLGNFIENHDNPRFAK	303		
QY	324	YTNDIALAKNVAAPFIILNDGPIIYAGOEQHYAGGNPDANREATWLSGYPTDSLYKLIA	383		
Db	304	YTDYSQAKNVLISYFISDGIPIVAGEEQHYAGGKVPYREATWLSGYDTSABLYTWIA	363		
QY	384	SANAIKNYAIKOTGFVYKNWPIYKDDTTIAMRKGTGSGQIVTILSNKASGDSYTLTSL	443		
Db	364	TTNAIRKLAIAADSAYITYANDAFYDTSNTIAMAKGTSGSQVITVLGNKSGSSSYTLTL	423		
QY	444	SGAGYTAGQQLTEVIGCTVTTVGSDGNVPVPMAGGLPRVLVYPTKLAGSKICSSS	498		
Db	424	SGSGYTTSGTKLIEAYTCTVTVDSGGDIPVPMASGLPRVLLIPASVVDSSSLCGGS	478		
RESULT 13					
Q9UV09 PRELIMINARY; PRT; 623 AA.					
ID	Q9UV09				
AC	Q9UV09				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Alpha-amylase.				
GN	Names=amvB;				
OS	Emeritella nidulans (Aspergillus nidulans).				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;				
OC	Eurotiales; Trichocomaceae; Emeritella.				
OX	NCBI_TaxID=162425;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Boase N.A., Murphy R.L., Kelly J.M.;				
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.				
DR	EMBL; AF082244; AAF17100.1; -				
DR	HSP; P56271; 2AAB.				
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.				
DR	GO; GO:0003824; F:catalytic activity; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR006047; Alpha_amyl_cat.				
DR	InterPro; IPR006589; Alp_amyl_cat_sub.				
DR	InterPro; IPR006046; Glyco_hydro_13.				
DR	Pfam; PF00128; Glyco_hydro_CBD.				
DR	Pfam; PF00128; Alpha-amylase; 1.				
DR	Pfam; PF00686; CBM_20; 1.				
DR	PRINTS; PR00110; ALPHAAMYLASE.				
DR	ProDom; PD001566; Glyco_hydro_CBD; 1.				
DR	SMART; SM00642; Amy; 1.				
SQ	SEQUENCE 623 AA; 69598 MW; 822F002C37F5A9A4 CRC64;				

Query Match 64.3%; Score 1725.5; DB 2; Length 623;
Best Local Similarity 63.7%; Pred. No. 1.4e-111;
Matches 309; Conservative 68; Mismatches 107; Indels 1; Gaps 1;

Qy	12	LOVAAPALAAATPAD-WRSQS	YIFLLTRDPARTDGS	TTATCNTADOKY	CGGTWQGIIDKLD	70		
Db	10	LALLGKAVHGLDAGWRSQS	YIFLLTRDPARTDGS	TAAACDLAQR	YCGGSGNOIINQLD	69		
Qy	71	YIQMGGTAIWIPTVTAQLPOT	TAYGDAYHGYWQODI	YSLAENYGTADDL	KALSALHER	130		
Db	70	YIQMGGTAIWIPTITEQIPDV	TAVGTGFHGYWQNI	YGVDTNLGTADDI	RALSEALHDR	129		
Qy	131	GMYLMDVVANHMGYD	GAGSVDSYVKPFRSSQD	YFHPFCFIONVEDO	TOVEDCWLGDMT	190		
Db	130	GMYLMDVVANHMSY	GPGGSTDTSIFTPFDS	SYFHSICALNNYD	NOQWENCFLGDDT	189		
Qy	191	VSLPDLDTTDDVKNNE	WDVGSVSNYSIDGLR	IDTVKHQKDFWP	GKNKAAGYVIGE	250		
Db	190	VSLTDLANTOSSEVRD	IWDWIEDIVANYSV	DGLRIDTVKHEK	DPWGYIDAAGYVSGE	249		
Qy	251	VLDGDPAYTCPYQNM	GVLMNYPYYPLLN	AFKSTSGSMDDL	YNNMINTVKS	DCPSTLLG	310	
Db	250	IFHGDPAITCPYQYD	MDGVNYPYYPLLN	AFKSSGMSDL	YNNMINTVAS	NCROPTLLG	309	
Qy	311	TFVENHDNPRPAS	TYNDIALAKNVA	AFIINDGPIIYAG	QEOHVAGGND	PANRATWLS	370	
Db	310	NFIENHDNPRPN	TYTDMSRAKNVA	FLUFLTDGPIV	YAGQEOHYSG	SNDPYNREFVMS	369	
Qy	371	GYPTDSELYKLI	ASANARINVAISK	DGFVYKKNWPI	VKDDTTIAMR	XGTDSQVTTLS	430	
Db	370	SYSTSSELYKF	AIATNKIRKUI	ASKDSYLS	TRNTPFYSDSN	YIAMRKGSGGVITLLN	429	
Qy	431	NKGASGDSY	TLSSLGAGYTACQ	QUTTEVIGCT	TVTVTSGDN	VPVPMAGGLPRVLY	PTEKLA	490
Db	430	NIGHTSIGSY	FDLYDHGYN	SANLVELYTCS	SVQVGSNGA	ISIPMTSGI	PLVLVPAAMWS	489
Qy	491	GSKTC	495					
Db	490	GSGLC	494					

RESULT 14	Q6YF33	PRELIMINARY;	PRT;	647 AA.
ID	Q6YF33			
AC	Q6YF33;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Alpha-amylase.			
OS	Lipomyces starkeyi.			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Lipomycetaceae; Lipomyces.			
OX	NCBI_TaxID:29829;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=KSM 22M;			
RX	PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;			
RA	Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,			
RA	Moore T.-W.;			
RT	"Cloning and expression of Lipomyces starkeyi alpha-amylase in			
RT	Escherichia coli and determination of some of its properties.";			
RL	FEMS Microbiol. Lett. 233:53-64(2004).			
DR	EMBL; AY155463; AN75021.1; -.			
DR	HSP; P26827; I447.			
DR	GO; GO:0004556; F.alpha-amylase activity; IEA.			
DR	GO; GO:0005975; P.carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha_amyl_cat.			
DR	InterPro; IPR006589; Alp_amyl_cat_sub.			
DR	InterPro; IPR005036; CBM_21.			
DR	Pfam; PF00128; Alpha-amylase; 1.			
DR	Pfam; PF03370; CBM_21; 1.			
DR	SMART; SM00642; Amy1; 1.			
SQ	SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;			
Query Match 61.9%; Score 1662; DB 2; Length 647;				
Best Local Similarity 61.4%; Pred. No. 3.8e-107;				

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Matches 298; Conservative 75; Mismatches 110; Indels 2; Gaps 1;
QY 12 LQVAAALAAATPADWRSSQSYFLLTRPARTDGTATACNADQKCGGTWQGIIDKLDY 71
Db 164 ISVSV--TGAANWRGRAIQYVTRFARTDGSITLYLCLDVTDRVYCGGSYQGINWLDY 221
QY 72 IQMGFTAIWTPVTAQLPOTTAAGDAYHGYWQDIYSLNENYGTADDLKALSSALHERG 131
Db 222 IQMGFTAIWISPIVENIPDDTGYGAYHYGWMKDFALMTNFGTADDLLALATELHNHG 281
QY 132 MYLMVDVVAHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFQIYBQTOVEDCWLGDNTV 191
Db 282 MYLMVDIVVNHFAFSGHADVDYSEYFPYSSQDYFHSFCWITDYSQTNVEQCMGDDTV 341
QY 192 SLPLDITDKVDVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCI 251
Db 342 PLVDVNTQLDVTAKSEYQSWQELIANYSIDGLRIDTVKHVQKDFWPAFQEAAGIYAV 401
QY 252 LDGDPATCYQNVMDGLNRYIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGT 311
Db 402 FDGDPSTCYQENLDGVLNYPYVPVSAFSGSVSSVSLVMDITLXSECTDTTLGSG 461
QY 312 FVENHNPFPASYNIDIALAKNVAFTIINDGIPPIYAGQEHYAGGNDPANREATWLSG 371
Db 462 FLENQNPFPSTVSDSLIKNAIAFTMLSDGPIIYQGEQGLNGNDPYNREALWLTG 521
QY 372 YPTDSLYKLJASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRGTDGSGQIVTILSN 431
Db 522 YSTSTFYKYIASLNQIRNAIQKDDTYLTQYQNWIVYSDSTTIAMRGKTGNQIIVLSN 581
QY 432 KGASGSYTLISGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGLPRVLYPTKLAG 491
Db 582 LGTSGSSSYTLTSLNTGTASSVVYELTCTAVTVDSGNLAVPMSSGLPKFVQESQLV 641
QY 492 SKICS 496
Db 642 SGICS 646

RESULT 15
AMYL LIPKO
ID AMYL LIPKO STANDARD; PRT; 624 AA.
AC Q0117;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2004 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase 1).
GN Name=LKAl;
OS Lipomyces kononenkoae.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Lipomycetaceae; Lipomyces.
OX NCBI_TaxID=34357;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IGC4052B;
RA MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;
RX Steyn A.J.C., Marmur J., Pretorius I.S.;
RT "Cloning, sequence analysis and expression in yeasts of a cDNA
RT containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";
RL Gene 166:65-71(1995).
RN [2]
RP SEQUENCE OF 29-44.
RC STRAIN=IGC4052B;
RX MEDLINE=96132108; PubMed=8593683;
RA Steyn A.J.C., Pretorius I.S.;
RT "Characterization of a novel alpha-amylase from Lipomyces kononenkoae
RT and expression of its gene (LKAl) in Saccharomyces cerevisiae.";
RL Curr. Genet. 28:526-533(1995).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
```

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -1- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
CC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U30376; AAC49622.1; ALT_INIT.
DR PIR; JC4510; JC4510.
DR HSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR005036; CBM_21.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF03370; CBM_21; 1.
DR SMART; SM00642; Aamy; 1.
DR KEGG; K01101; Amy1; 1.
KW Calcium-binding; Carbohydrate metabolism; Direct protein sequencing;
KW Glycoprotein; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 624 Alpha-amylase 1.
FT DOMAIN 40 133 Carbohydrate binding type-21.
FT ACT_SITE 353 353 Nucleophile (By similarity).
FT ACT_SITE 377 377 Proton donor (By similarity).
FT ACT_SITE 444 444 By similarity.
FT METAL 268 268 Calcium 1 (By similarity).
FT METAL 309 309 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 322 322 Calcium 1 (By similarity).
FT METAL 353 353 Calcium 2 (By similarity).
FT METAL 357 357 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 377 377 Calcium 2 (By similarity).
FT DISULFID 177 185 By similarity.
FT DISULFID 297 311 By similarity.
FT DISULFID 387 430 By similarity.
FT DISULFID 587 622 By similarity.
FT CARBOHYD 304 304 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 344 344 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 624 AA; 68876 MW; 87EB16534F5A9A9F CRC64;

Query Match 60.7%; Score 1629; DB 1; Length 624;
Best Local Similarity 60.6%; Pred No. 7.1e-105;
Matches 292; Conservative 77; Mismatches 113; Indels 0; Gaps 0;

QY 15 AAPALAAATPADWRSSQSYFLLTRPARTDGTATACNADQKCGGTWQGIIDKLDYIQG 74
Db 142 SASVPTGTAANWRGSIYQVVTDRPARTDGSITLYLCLDVTDRVYCGGSYQGINWLDYIQG 201
QY 75 MGFTAIWTPVTAQLPOTTAAGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYL 134
Db 202 MGFTAIWISPIVENIPDDTGYGAYHYGWMKDFALMTNFGTADDLLALATELHNRMYL 261
QY 135 MYDVVANMGYDGAGSSVDYSVFKPFSSQDYFHPFCFQIYBQTOVEDCWLGDNTVSLP 194
Db 262 MYDIVVNHFAFSGHADVDYSEYFPYSSQDYFHSFCWITDYSQTNVEQCMGDDSDVPLV 321
QY 195 DLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCI 254
Db 322 DVNTQLDVTAKSEYQSWQELIANYSIDGLRIDTVKHVQKDFWPAFQEAAGIYVGEVFDG 381
QY 255 DPATYCPQNVMDGLNRYIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVE 314
Db 382 DPSYTCYQENLDGVLNYPYVPVSAFSGSVSSVSLVMDITLXSECTDTTLGSGFLE 441
QY 315 NHDNPRFASYNIDIALAKNVAFTIINDGIPPIYAGQEHYAGGNDPANREATWLSGYPT 374
Db 442 NODNPRFSPSTVSDSLIKNAIAFTIISDGIPIIYQGEQGLNGNDPYNREALWPTGYST 501
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OM protein - protein search, using sw model

Run on: November 7, 2005, 17:47:24 ; Search time 74.9884 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2

Perfect score: 2684

Sequence: 1 MWAWSLFLYGLQVAAPALA.....LPRVLYPTKLAGSKICSSS 498

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents 'AA':*

- 1: /cgn2_6/ptodata/1/1aa/5A COMB pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B COMB pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A COMB pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B COMB pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS COMB pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2572	95.8	478	1	US-08-720-899-7
2	2572	95.8	478	1	US-08-459-610-7
3	2572	95.8	478	2	US-08-343-804-7
4	2572	95.8	478	2	US-08-600-908A-10
5	2572	95.8	478	3	US-08-683-838A-10
6	2572	95.8	478	3	US-09-182-859-7
7	2572	95.8	478	4	US-09-672-459-7
8	2572	95.8	478	4	US-09-636-252A-10
9	2572	95.8	478	4	US-10-186-042-7
10	2503.5	93.3	478	2	US-08-339-715A-2
11	1392	51.9	468	1	US-08-470-702-6
12	1392	51.9	468	1	US-08-467-831-6
13	1391	51.8	468	1	US-08-204-656B-4
14	1391	51.8	468	1	US-08-470-702-7
15	1391	51.8	468	1	US-08-467-831-7
16	1388	51.7	468	1	US-08-204-656B-6
17	1388	51.7	468	1	US-08-470-702-8
18	1388	51.7	468	1	US-08-467-831-8
19	1387	51.7	468	1	US-08-204-656B-2
20	1387	51.7	468	1	US-08-204-656B-8
21	1387	51.7	468	1	US-08-470-702-9
22	1387	51.7	468	1	US-08-467-831-9
23	450	16.8	719	3	US-09-386-607-2
24	450	16.8	719	4	US-09-645-707B-2
25	446	16.6	686	3	US-08-947-965-73
26	444	16.5	685	3	US-08-947-965-72
27	428.5	16.0	655	1	US-08-469-202-28

28	428.5	16.0	655	2	US-08-484-434C-35	Sequence 35, Appl
29	428.5	16.0	655	4	US-09-384-361-35	Sequence 35, Appl
30	427.5	15.9	655	1	US-08-469-202-27	Sequence 27, Appl
31	427.5	15.9	655	4	US-08-484-434C-34	Sequence 34, Appl
32	427.5	15.9	655	4	US-09-384-361-34	Sequence 34, Appl
33	426.5	15.9	683	3	US-08-947-965-2	Sequence 2, Appl
34	421.5	15.7	624	3	US-08-947-965-78	Sequence 78, Appl
35	418	15.6	676	3	US-08-947-965-71	Sequence 71, Appl
36	413	15.4	686	3	US-08-947-965-70	Sequence 70, Appl
37	413	15.4	687	3	US-08-947-965-75	Sequence 75, Appl
38	404.5	15.1	833	3	US-09-514-302-3	Sequence 3, Appl
39	404.5	15.1	833	4	US-10-014-436-3	Sequence 3, Appl
40	404.5	15.1	1938	3	US-09-514-302-2	Sequence 2, Appl
41	404.5	15.1	1938	4	US-10-014-436-2	Sequence 2, Appl
42	398	14.8	685	3	US-08-947-965-74	Sequence 74, Appl
43	396	14.8	675	3	US-08-947-965-76	Sequence 76, Appl
44	385.5	14.4	680	3	US-08-947-965-77	Sequence 77, Appl
45	370	13.8	588	2	US-08-339-715A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Biesgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-Oct-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-720-899-7

Query Match 95.8%; Score 2572; DB 1; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDIYIQGMGFTAI 80
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Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDIYIQGMGFTAI 60
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QY 81 WITPVTQAQLPQTAYGDAYHGVTWQODIYSLNENYGTADDLKSALHERGMYLMDVVA 140
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Db 61 WITPVTQAQLPQTAYGDAYHGVTWQODIYSLNENYGTADDLKSALHERGMYLMDVVA 120
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QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYVEDQTVQEDCWLGDNVTSLPDLDTTK 200
| | | | |
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYVEDQTVQEDCWLGDNVTSLPDLDTTK 180
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QY 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCI GEVL DGPAYTC 260
| | | | |
Db 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCI GEVL DGPAYTC 240
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Db 301 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEHYAGGNDPANREATWLSGPTDSELYK 360
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Db 361 LIASANAIRNYAISKDTGFTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
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QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
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Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478
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RESULT 2

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US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match          95.8%; Score 2572; DB 1; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDIYIQGMGFTAI 80
| | | | |
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKYCGGTWQGIIDKLDIYIQGMGFTAI 60
| | | | |
QY 81 WITPVTQAQLPQTAYGDAYHGVTWQODIYSLNENYGTADDLKSALHERGMYLMDVVA 140
| | | | |
Db 61 WITPVTQAQLPQTAYGDAYHGVTWQODIYSLNENYGTADDLKSALHERGMYLMDVVA 120
| | | | |
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYVEDQTVQEDCWLGDNVTSLPDLDTTK 200
| | | | |
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYVEDQTVQEDCWLGDNVTSLPDLDTTK 180
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QY 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCI GEVL DGPAYTC 260
| | | | |
Db 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCI GEVL DGPAYTC 240
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| | | | |
Db 241 PYQNVMDGVLNYPYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGTFVENHNDNPR 300
| | | | |
QY 321 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEHYAGGNDPANREATWLSGPTDSELYK 380
| | | | |
Db 301 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEHYAGGNDPANREATWLSGPTDSELYK 360
| | | | |
QY 381 LIASANAIRNYAISKDTGFTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
| | | | |
Db 361 LIASANAIRNYAISKDTGFTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
| | | | |
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 498
| | | | |
Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPMAGGLPRVLYPTEKLAGSKICSSS 478
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RESULT 3

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US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
```

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;
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-343-804-7

Query Match          95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 ATPADWRSQSIYFLLTDRFARTDGSSTATCNCTADQKCGGTWQGIIDKLDIYIQMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTATCNCTADQKCGGTWQGIIDKLDIYIQMGFTAI 60
Qy 81 WITPVTAQLPQTAYGDYAHGYWQODIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTAQLPQTAYGDYAHGYWQODIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
Qy 141 NHMGYDGAGSSVDYSVPKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVPKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTIVKHQKDFWPGYNKAAGYICIGEVLGDGPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTIVKHQKDFWPGYNKAAGYICIGEVLGDGPAYTC 240
Qy 261 PYQNVMDGVNLNPIYYFLNNAFKSTSGMDDLNNMINTVKSDDCPDSTLLGTFVFNHNDNPR 320
Db 241 PYQNVMDGVNLNPIYYFLNNAFKSTSGMDDLNNMINTVKSDDCPDSTLLGTFVFNHNDNPR 300
Qy 321 FASYTNDIALAKNVAAPFIILNDGIPITIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAPFIILNDGIPITIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
Qy 381 LIASANAIRNYAISKDTGFVYKWPPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNYAISKDTGFVYKWPPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
Qy 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 4
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: "-Amylase Mutants
; NUMBER OF SEQUENCE ADDRESSES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 5989169 No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394,204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-600-908A-10

Query Match 95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSSQSYELLTDRFARTDGSSTATCNTADQKCYCGGTWGGIIDLKLDYIQMGFTAI 80
DB 1 ATPADWRSSQSYELLTDRFARTDGSSTATCNTADQKCYCGGTWGGIIDLKLDYIQMGFTAI 60

QY 81 WITPVTQAQLPQTAYGDAVHGYYQQDIYSLNENYGTADDLKALSSALHERGMYLWMDVVA 140
DB 61 WITPVTQAQLPQTAYGDAVHGYYQQDIYSLNENYGTADDLKALSSALHERGMYLWMDVVA 120

QY 141 NHMGYDGAGSSVDYVPKPFSSQDYFHPFCFIQNYEDQQTQVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDGAGSSVDYVPKPFSSQDYFHPFCFIQNYEDQQTQVEDCWLGDNTVSLPDLDTTK 180

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQVQDFWPGYNKAAGVYCI GEVLGDGPAYTC 260
DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQVQDFWPGYNKAAGVYCI GEVLGDGPAYTC 240

QY 261 PYQVNMVGVNLPIYPTPLNNAFKSTGSGMDDLNMINTVKSDCPDSTLLGTFFVENHDNPR 320
DB 241 PYQVNMVGVNLPIYPTPLNNAFKSTGSGMDDLNMINTVKSDCPDSTLLGTFFVENHDNPR 300

QY 321 FASYTNDIALAKNVAAPFIILNDGIPYIYAGQEQHYAGGNDPANREATWLSGYPTDSLYK 380
DB 301 FASYTNDIALAKNVAAPFIILNDGIPYIYAGQEQHYAGGNDPANREATWLSGYPTDSLYK 360

QY 381 LIASANAIRNAYIAISKDTGFYTKWPIYKDDTTIAMRKGTGDSQIVTILSNKGSAGDSYT 440
DB 361 LIASANAIRNAYIAISKDTGFYTKWPIYKDDTTIAMRKGTGDSQIVTILSNKGSAGDSYT 420

QY 441 LSLSGAGYTAGQQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTPEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGQQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTPEKLAGSKICSSS 478

RESULT 5
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Big rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401

```

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; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394,204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-600-908A-10

Query Match 95.8%; Score 2572; DB 2; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSSQSIYELLTDRFARTDGSSTATCNTADQKCYCGGTWGGIIDLKLDYIQMGFTAI 80
DB 1 ATPADWRSSQSIYELLTDRFARTDGSSTATCNTADQKCYCGGTWGGIIDLKLDYIQMGFTAI 60

QY 81 WITPVTQAQLPQTAYGDAVHGYYQQDIYSLNENYGTADDLKALSSALHERGMYLWMDVVA 140
DB 61 WITPVTQAQLPQTAYGDAVHGYYQQDIYSLNENYGTADDLKALSSALHERGMYLWMDVVA 120

QY 141 NHMGYDGAGSSVDYVPKPFSSQDYFHPFCFIQNYEDQQTQVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDGAGSSVDYVPKPFSSQDYFHPFCFIQNYEDQQTQVEDCWLGDNTVSLPDLDTTK 180

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQVQDFWPGYNKAAGVYCI GEVLGDGPAYTC 260
DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQVQDFWPGYNKAAGVYCI GEVLGDGPAYTC 240

QY 261 PYQVNMVGVLYPIYPTLLNAFSTSGSMDLLYNMINTVKSDCPDSTLLGTFFVENHDNPR 320
DB 241 PYQVNMVGVLYPIYPTLLNAFSTSGSMDLLYNMINTVKSDCPDSTLLGTFFVENHDNPR 300

QY 321 FASYTNDIALAKNVAAPFIILNDGIPYIYAGQEQHYAGGNDPANREATWLSGYPTDSLYK 380
DB 301 FASYTNDIALAKNVAAPFIILNDGIPYIYAGQEQHYAGGNDPANREATWLSGYPTDSLYK 360

QY 381 LIASANAIRNYAISKDTGFYTKWPIYKDDTTIAMRKGTGDSQIVTILSNKSGASGSY 440
DB 361 LIASANAIRNYAISKDTGFYTKWPIYKDDTTIAMRKGTGDSQIVTILSNKSGASGSY 420

QY 441 LSLSGAGYTAGQQQLTEVIGCTTTVGSDGNVPVPMAGGLPRVLYPTKLAGSKICSSS 498
DB 421 LSLSGAGYTAGQQQLTEVIGCTTTVGSDGNVPVPMAGGLPRVLYPTKLAGSKICSSS 478

RESULT 5
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Big rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: "-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60227240 No. 60227240disk of No. 60227240 America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-683-838A-10

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Query Match          95.8%; Score 2572; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120

QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNVTSPLDITTK 200
Db 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNVTSPLDITTK 180

QY 201 DVVKNEWYDWGSLVSNYSIDGLRDTVKHVKQDFWPGYNKAAGVYCI GEVLGDGPATC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRDTVKHVKQDFWPGYNKAAGVYCI GEVLGDGPATC 240

QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 320
Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 300

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSLEYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSLEYK 360

QY 381 LIASANAIRNVAISKDTGFTYKWPYKDDITIAMRKGTGDSQIIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNVAISKDTGFTYKWPYKDDITIAMRKGTGDSQIIVTILSNKGASGDSYT 420

QY 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSS 498
Db 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSS 478

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RESULT 6
US-09-182-859-7
; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik

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; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7

Query Match          95.8%; Score 2572; DB 3; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120

QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNVTSPLDITTK 200
Db 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNVTSPLDITTK 180

QY 201 DVVKNEWYDWGSLVSNYSIDGLRDTVKHVKQDFWPGYNKAAGVYCI GEVLGDGPATC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRDTVKHVKQDFWPGYNKAAGVYCI GEVLGDGPATC 240

QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 320
Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 300

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSLEYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSLEYK 360

QY 381 LIASANAIRNVAISKDTGFTYKWPYKDDITIAMRKGTGDSQIIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNVAISKDTGFTYKWPYKDDITIAMRKGTGDSQIIVTILSNKGASGDSYT 420

QY 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSS 498
Db 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSS 478

RESULT 7
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30

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; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PR1
; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match 95.8%; Score 2572; DB 4; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
DB 61 WITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120

QY 141 NMGYDGAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
DB 121 NMGYDGAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 180

QY 201 DVVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGVLDGDPAYTC 260
DB 181 DVVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGVLDGDPAYTC 240

QY 261 PYQNVMDGVLNPIYIYPLNAPKSTSGSMDLLYNNINTVKS DCPDSTLLGTFFVENHNDPR 320
DB 241 PYQNVMDGVLNPIYIYPLNAPKSTSGSMDLLYNNINTVKS DCPDSTLLGTFFVENHNDPR 300

QY 321 FASYTNDIALAKNVAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSLYK 380
DB 301 FASYTNDIALAKNVAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSLYK 360

QY 381 LIASANAIRNVAISKDTGFVTKNPIYKDDTTIARKGTGDSQIIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNVAISKDTGFVTKNPIYKDDTTIARKGTGDSQIIVTILSNKGASGDSYT 420

QY 441 LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 8
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/09/636, 252A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683, 838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PR1
; ORGANISM: A. oryzae
US-09-636-252A-10

Query Match 95.8%; Score 2572; DB 4; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRPARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 140
DB 61 WITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLMDVVA 120

QY 141 NMGYDGAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
DB 121 NMGYDGAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 180

QY 201 DVVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGVLDGDPAYTC 260
DB 181 DVVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGVLDGDPAYTC 240

QY 261 PYQNVMDGVLNPIYIYPLNAPKSTSGSMDLLYNNINTVKS DCPDSTLLGTFFVENHNDPR 320
DB 241 PYQNVMDGVLNPIYIYPLNAPKSTSGSMDLLYNNINTVKS DCPDSTLLGTFFVENHNDPR 300

QY 321 FASYTNDIALAKNVAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSLYK 380
DB 301 FASYTNDIALAKNVAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSLYK 360

QY 381 LIASANAIRNVAISKDTGFVTKNPIYKDDTTIARKGTGDSQIIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNVAISKDTGFVTKNPIYKDDTTIARKGTGDSQIIVTILSNKGASGDSYT 420

QY 441 LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
DB 421 LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 9
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186, 042
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672, 459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182, 859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PR1
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 95.8%; Score 2572; DB 4; Length 478;
Best Local Similarity 99.8%; Pred. No. 3.2e-220;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGWQODIYSLNENYGTADDLKSALSSALHERGMYLMDVVA 140
DB 61 WITPVTAQLPQTAYGDAYHGWQODIYSLNENYGTADDLKSALSSALHERGMYLMDVVA 120
QY 141 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTOVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTOVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGMDDLNNMINTVKS DCPDSTLLGTFFVENHNDNR 320
DB 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGMDDLNNMINTVKS DCPDSTLLGTFFVENHNDNR 300
QY 321 FASYTNDIALAKNVAFAFIILNDGPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAFAFIILNDGPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFVTKNPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNVAISKDTGFVTKNPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSS 498
DB 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSS 478

RESULT 10

US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriki, Takashi
; APPLICANT: Yanase, Michio
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; TITLE OF INVENTION: NEOPULLULANASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSER: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; STREET: G. Street
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Melser, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-715A-2

Query Match 93.3%; Score 2503.5; DB 2; Length 478;
Best Local Similarity 97.9%; Pred. No. 4e-214;
Matches 468; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 21 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGWQODIYSLNENYGTADDLKSALSSALHERGMYLMDVVA 140
DB 61 WITPVTAQLPQTAYGDAYHGWQODIYSLNENYGTADDLKSALSSALHERGMYLMDVVA 120
QY 141 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTOVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIONYEDQTOVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGMDDLNNMINTVKS DCPDSTLLGTFFVENHNDNR 320
DB 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGMDDLNNMINTVKS DCPDSTLLGTFFVENHNDNR 300
QY 321 FASYTNDIALAKNVAFAFIILNDGPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAFAFIILNDGPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFVTKNPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 440
DB 361 LIASANAIRNVAISKDTGFVTKNPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 419
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSS 498
DB 420 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSS 477

RESULT 11
US-08-470-702-6
; Sequence 6, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/470, 702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-470-702-6

Query Match 51.9%; Score 1392; DB 1; Length 468;
Best Local Similarity 54.4%; Pred. No. 3.1e-115;
Matches 259; Conservative 81; Mismatches 126; Indels 10; Gaps 5;

QY 22 TPAD-WRSQSIYFLLTDRPARTGTTATCNTADQKYGCGTGWQIIDKLDYIQGMGFTAI 80
DB 2 TNADKWRSSQSIYQIVTDRPARTGDTTSACNTEDRLYCGSGFQGIKKLDYIKDMGFTAI 61

QY 81 WITPVTAQLPOTTAYGDAYHYGWOQDIYSLNENYGTADDLKALSSALHERGMVLMVDVVA 140
DB 62 WISPVVENIPDNTAYGYAHGFWMKNIYKINENFGTADDLKSLAQELHHRDMLLMVDIVT 121

QY 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVTSLPDLDTTK 200
DB 122 NHYSGDSGSDSIDSEYTPFPNDQKYFHNKCLISNYDDQAQVQSCWEGSSVALPDLRTD 181

QY 201 DVVKNWYDVGSLVNSYIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 182 SDVASVFNWVKDFVGNYSIDGLRIDSAKHVDQGFPPDFVSAGSVYSGVEVFGQDPAYTC 241

QY 261 PYQNVMDGVNLNPIYYPYLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTFVENHNDNR 320
DB 242 PYQNYIPGVSNYPLIYPTTRFPKTTDSSSELQMISSVASSCSDPTLLTNFVENHNDNR 301

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 302 FASMTSDQSLSISNAIAFVLLGDGIPVIYVYQEGQLSGKSDPNNREALWLSGYNKESDYK 361

QY 381 LIASANAIRNVAISKDTGFTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASDSYT 440
DB 362 LIAKANAARNAAYQDSSYATSQLSVIFSNHVIATKRGS----VVSFNNLGSSGS-D 416

QY 441 LSLSGAGYTAGOQLTEVIGCTTVTGVSGDGNVPVPMAGGLPRVLVPTPEKLAGSKICS 496
DB 417 VTISNTGYSGEDLVEVLCTSVSGSSD--LQVSIQGGQGPQIFVPAK--YASDICS 468

RESULT 12
US-08-467-831-6
; Sequence 6, Application US/08467831
; Patent No. 5635378
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
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QY 441 LSLGAGYTAGOOLTEVIGCTTVTGVSDGNVPMAGGLPRVLVPTKLAGSKICS 496
Db 417 VTISNTGYSGEDLVEVLTCSTVSGSSD--LQVSIQGGOPQIFVPAK--YASDICS 468

RESULT 13
US-08-204-656B-4
; Sequence 4, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuo
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-204-656B-4

Query Match 51.8%; Score 1391; DB 1; Length 468;
Best Local Similarity 54.4%; Pred. No. 3.8e-115;
Matches 259; Conservative 81; Mismatches 126; Indels 10; Gaps 5;

QY 22 TPAD-WRSQSIYQIVTDRFARTDGTSTATCNADQKYGCGTWQGIIDKLDYIQMGFTAI 80
Db 2 TNADKWRQSIYQIVTDRFARTDGTSTATCNADQKYGCGTWQGIIDKLDYIQMGFTAI 61

QY 81 WTPVTAQLPQTAYGDYVHGVQODIYSLNENYGTADDLKALSALHERGMYLMDVVA 140
Db 62 WISPVVENIPDNTAYGYAHGWMKNIYKINENFGTADDLKSLAQELHDMMLMDIVT 121

QY 141 NHMGYDGGAGSDYDVFPFSSDYFPCFNTQVEDQVDCWLGNTVSLPLDITTK 200
Db 122 NHYSGDGGSDSIDYSEYTFPFNDQKQYFHNKYLISNTDQDQVQSCWEGSSVALPLRTED 181

QY 201 DVVKNEDWVNGSLVSNYSIDGLRDTVKGHVOKDFWPKYKNAAGYVCIGELVDGDPATVC 260
Db 182 SDVASVENSVKWDFVGNYSIDGLRIDSAGKVDQGFDFVFSAGSYVSGVEFGQDPATVC 241

QY 261 PYQNVMDGVNLPIYIYPLLNAPKFTSGSMDDLYNNMINTVKSDPCDPSTLLGTFVENDNPR 320
Db 2 TNADKWRQSIYQIVTDRFARTDGTSTATCNADQKYGCGTWQGIIDKLDYIQMGFTAI 61

Db 242 PYQNIYPGVSNVPLYYTTRPEKTTDSSSELTOMISSVASSCSDPTLLTNFVENHDNER 301
QY 321 FASYTNDIALAKNVAAPFIILNDGIPILYAGQBOHYAGNDPANREATWLSGYPTSELYK 380
Db 302 FASMTSDQSLSNATAFVLLGDIPIVYIYQBGSLSGKSDPNRNREALWLSGYNKESDYK 361

QY 381 LIASANAIRNVAISKDTGTFVTYKKNPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
Db 362 LIAKANAARNAAVQDSSYATSQLSVIFSNDRHVIATKGS-----VVSFNNLGSQSS-D 416

QY 441 LSLGAGYTAGOOLTEVIGCTTVTGVSDGNVPMAGGLPRVLVPTKLAGSKICS 496
Db 417 VTISNTGYSGEDLVEVLTCSTVSGSSD--LQVSIQGGOPQIFVPAK--YASDICS 468

RESULT 14
US-08-470-702-7
; Sequence 7, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-470-702-7

Query Match 51.8%; Score 1391; DB 1; Length 468;
Best Local Similarity 54.4%; Pred. No. 3.8e-115;
Matches 259; Conservative 81; Mismatches 126; Indels 10; Gaps 5;

QY 22 TPAD-WRSQSIYQIVTDRFARTDGTSTATCNADQKYGCGTWQGIIDKLDYIQMGFTAI 80
Db 2 TNADKWRQSIYQIVTDRFARTDGTSTATCNADQKYGCGTWQGIIDKLDYIQMGFTAI 61
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:11:05 ; Search time 270.151 Seconds
(without alignments)
771.303 Million cell updates/sec

Title: US-10-820-200-2

Perfect score: 2684

Sequence: 1 MVANWSFLYGLQVAAPALA.....LPRVLYPTKLAGSKICSSS 498

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/ECTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2684	100.0	498	16	US-10-820-200-2
2	2684	100.0	498	17	US-10-877-849-30
3	2684	100.0	499	16	US-10-797-393A-5
4	2884	100.0	608	17	US-10-877-849-40
5	2684	100.0	640	17	US-10-877-849-36
6	2674	99.6	499	16	US-10-815-495-18
7	2662	99.2	498	16	US-10-815-495-22
8	2572	95.8	478	14	US-10-184-771-10
9	2572	95.8	478	14	US-10-186-042-7
10	2572	95.8	478	15	US-10-644-187-7
11	2572	95.8	478	17	US-10-926-720-10

12	2572	95.8	478	17	US-10-980-759-7	Sequence 7, Appli
13	2572	95.8	478	20	US-11-064-196-10	Sequence 10, Appl
14	2570	95.8	476	17	US-10-877-849-43	Sequence 43, Appl
15	2569	95.7	1095	14	US-10-228-063-45	Sequence 45, Appl
16	2100	78.2	495	14	US-10-213-990-42	Sequence 42, Appl
17	2012	75.0	494	17	US-10-486-868-13	Sequence 13, Appl
18	1835	68.4	630	14	US-10-213-990-45	Sequence 45, Appl
19	1810	67.4	640	17	US-10-877-007-22	Sequence 22, Appl
20	1810	67.4	640	17	US-10-877-849-41	Sequence 41, Appl
21	1798	67.0	505	17	US-10-877-849-42	Sequence 42, Appl
22	1798	67.0	511	17	US-10-877-849-38	Sequence 8, Appli
23	1798	67.0	609	17	US-10-877-849-38	Sequence 38, Appl
24	1798	67.0	629	17	US-10-877-849-34	Sequence 34, Appl
25	1798	67.0	640	17	US-10-877-849-32	Sequence 32, Appl
26	1778	66.2	484	15	US-10-416-393-1	Sequence 1, Appli
27	1778	66.2	484	16	US-10-797-393A-1	Sequence 18, Appl
28	1214.5	45.2	547	14	US-10-213-990-48	Sequence 48, Appl
29	1183	44.1	555	17	US-10-486-868-15	Sequence 15, Appl
30	1163	43.3	567	17	US-10-486-868-18	Sequence 18, Appl
31	1160	43.2	500	15	US-10-369-493-12469	Sequence 12469, A
32	1085	40.4	549	17	US-10-486-868-14	Sequence 2223, Ap
33	1015.5	37.8	513	15	US-10-369-493-2223	Sequence 22679, A
34	898.5	33.5	564	15	US-10-369-493-22679	Sequence 22723, A
35	873	32.5	493	15	US-10-369-493-22723	Sequence 291647,
36	651	24.3	263	16	US-10-425-115-291647	Sequence 108, App
37	541	20.2	502	14	US-10-081-872-108	Sequence 108, App
38	541	20.2	502	15	US-10-385-305-108	Sequence 19940, A
39	483.5	18.0	547	15	US-10-369-493-19940	Sequence 4, Appli
40	480.5	17.9	547	15	US-10-369-493-19062	Sequence 2, Appli
41	456.5	17.0	713	17	US-10-504-543-4	Sequence 2, Appli
42	450	16.8	719	14	US-10-234-266-2	Sequence 2, Appli
43	450	16.8	719	15	US-10-442-558-2	Sequence 2, Appli
44	450	16.8	719	15	US-10-453-828-2	Sequence 2, Appli
45	450	16.8	719	20	US-11-048-000-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Pedersen, Sven
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match	100.0%	Score 2684	DB 16	Length 498
Best Local Similarity	100.0%	Pred. No. 2.7e-213		
Matches 498	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MVANWSFLYGLQVAAPALAAPADWRSQSIYFLITDREPARTDGTGTTATCNADQKYCGG	60	
Db	1	MVANWSFLYGLQVAAPALAAPADWRSQSIYFLITDREPARTDGTGTTATCNADQKYCGG	60	
Qy	61	THQGIIDKLDYICGGFTAIWITPTAQLPOTAYGVQODIYSLNENYGTADDL	120	

Db 61 TWQGIIDKLDYIQGMGFTAIWITPVAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Qy 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
Db 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
Qy 181 VEDCWLGNVSLPDLDTTKDVKVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
Db 181 VEDCWLGNVSLPDLDTTKDVKVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
Qy 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVLYNPIYYPILLNAPKSTSGSMDDLNNINTVK 300
Db 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVLYNPIYYPILLNAPKSTSGSMDDLNNINTVK 300
Qy 301 SDPCPSTLLGTFFVENHNDPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQSOHYAGGND 360
Db 301 SDPCPSTLLGTFFVENHNDPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQSOHYAGGND 360
Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
Db 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
Qy 421 DGSQIVTILSNKGAGSDSYTILSLGAGYTAGQQLTEVIGCTTIVTSGDGNVVPVPMAGGLP 480
Db 421 DGSQIVTILSNKGAGSDSYTILSLGAGYTAGQQLTEVIGCTTIVTSGDGNVVPVPMAGGLP 480
Qy 481 RVLYPEKLAGSKICSSS 498
Db 481 RVLYPEKLAGSKICSSS 498
RESULT 2
US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match 100.0%; Score 2684; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.7e-213;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNADQKCGG 60
Db 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNADQKCGG 60
Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Db 61 TWQGIIDKLDYIQGMGFTAIWITPVAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Qy 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
Db 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
Qy 181 VEDCWLGNVSLPDLDTTKDVKVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
Db 181 VEDCWLGNVSLPDLDTTKDVKVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240

Qy 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVLYNPIYYPILLNAPKSTSGSMDDLNNINTVK 300
Db 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVLYNPIYYPILLNAPKSTSGSMDDLNNINTVK 300
Qy 301 SDPCPSTLLGTFFVENHNDPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQSOHYAGGND 360
Db 301 SDPCPSTLLGTFFVENHNDPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQSOHYAGGND 360
Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
Db 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
Qy 421 DGSQIVTILSNKGAGSDSYTILSLGAGYTAGQQLTEVIGCTTIVTSGDGNVVPVPMAGGLP 480
Db 421 DGSQIVTILSNKGAGSDSYTILSLGAGYTAGQQLTEVIGCTTIVTSGDGNVVPVPMAGGLP 480
Qy 481 RVLYPEKLAGSKICSSS 498
Db 481 RVLYPEKLAGSKICSSS 498
RESULT 3
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Feister, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5
Query Match 100.0%; Score 2684; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.7e-213;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNADQKCGG 60
Db 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRPARTDGSSTTATCNADQKCGG 61
Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVAQLPQTAYGDAYHGYWQODIYSLNENYGTADDL 121
Qy 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
Db 122 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 181
Qy 181 VEDCWLGNVSLPDLDTTKDVKVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
Db 182 VEDCWLGNVSLPDLDTTKDVKVKNWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 241
Qy 241 KAAGVYCI GEVLGDGPAYTCYQNVMDGVLYNPIYYPILLNAPKSTSGSMDDLNNINTVK 300
Db 242 KAAGVYCI GEVLGDGPAYTCYQNVMDGVLYNPIYYPILLNAPKSTSGSMDDLNNINTVK 301
Qy 301 SDPCPSTLLGTFFVENHNDPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQSOHYAGGND 360
Db 302 SDPCPSTLLGTFFVENHNDPRFASVTNDIALAKNVAAPFIILNDGIPIIYAGQSOHYAGGND 361
Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 420
Db 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRKG 421

[illegible]

RESULT 4

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US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vlasov-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

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Query Match	100.0%; Score 2684; DB 17; Length 608;
Best Local Similarity	100.0%; Pred. No. 3.5e-213;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MVAWWSLFLYGLQVAAPALANPADWRSQSIFLLTDRFARTDGSSTTACTADQKYCGG 60
Db	1 MVAWWSLFLYGLQVAAPALANPADWRSQSIFLLTDRFARTDGSSTTACTADQKYCGG 60
Qy	61 TWQGIIDKLDYIQCMGFTAIWITPTVTAQLPOTTAAGDAYHGYWOODIYLSLNNYGTADDL 120
Db	61 TWQGIIDKLDYIQCMGFTAIWITPTVTAQLPOTTAAGDAYHGYWOODIYLSLNNYGTADDL 120
Qy	121 KALSSALHERGMYLMDVAVNMGYDAGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
Db	121 KALSSALHERGMYLMDVAVNMGYDAGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
Qy	181 VEDCWLGDNTVSLPDLDTTKDVKVNEWYDWMYGSLSVNSYSIDGLRIDTVKHVKQDFWPGYN 240
Db	181 VEDCWLGDNTVSLPDLDTTKDVKVNEWYDWMYGSLSVNSYSIDGLRIDTVKHVKQDFWPGYN 240
Qy	241 KAAGVYCI GEVL DGDPA YTC PYQNVMDGV LNP IYYP LLNAFKSTSGSMDLLYNNIMTVK 300
Db	241 KAAGVYCI GEVL DGDPA YTC PYQNVMDGV LNP IYYP LLNAFKSTSGSMDLLYNNIMTVK 300
Qy	301 SDCPDSTLLGTFVFNHONPRFASVTNDIALAKNVAAPFIILNDGIPILIYAGOEQHYAGND 360
Db	301 SDCPDSTLLGTFVFNHONPRFASVTNDIALAKNVAAPFIILNDGIPILIYAGOEQHYAGND 360
Qy	361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKWPYIKDDTTTAMRKG 420
Db	361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKWPYIKDDTTTAMRKG 420
Qy	421 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQITEVIGCTTVTVSGDGNVPVPMAGGLP 480
Db	421 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQITEVIGCTTVTVSGDGNVPVPMAGGLP 480
Qy	481 RVLYPTTEKLAGSKITCSSS 498

RESULT 6

US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1

```
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match          99.6%; Score 2674; DB 16; Length 499;
Best Local Similarity 99.6%; Pred. No. 1.8e-212;
Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCYGG 60
DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCYGG 61
QY 61 TWQGIIDKLDYIQGNGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGNGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 121
QY 121 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241
QY 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLYNNINTVK 300
DB 242 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLYNNINTVK 301
QY 301 SDPCDSTLLGTFFVENHNDNPFASVTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGND 360
DB 302 SDPCDSTLLGTFFVENHNDNPFASVTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 421
QY 421 DGSQIVTILSKNGASGDSYTLISLGSAGYTAGOQLTEVIGCTTVTVGSGNVVPVMAGGLP 480
DB 422 DGSQIVTILSKNGASGDSYTLISLGSAGYTAGOQLTEVIGCTTVTVGSGNVVPVMAGGLP 481
QY 481 RVLYPEKLAGSKICSS 498
DB 482 RVLYPEKLAGSKICSS 499

RESULT 7
US-10-815-495-22
; Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 22
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match          99.2%; Score 2662; DB 16; Length 498;
Best Local Similarity 99.6%; Pred. No. 1.8e-211;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCYGG 60
DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCYGG 61
QY 61 TWQGIIDKLDYIQGNGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGNGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 121
QY 121 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241
QY 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLYNNINTVK 300
DB 242 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLYNNINTVK 301
QY 301 SDPCDSTLLGTFFVENHNDNPFASVTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGND 360
DB 302 SDPCDSTLLGTFFVENHNDNPFASVTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 420
DB 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 421
QY 421 DGSQIVTILSKNGASGDSYTLISLGSAGYTAGOQLTEVIGCTTVTVGSGNVVPVMAGGLP 480
DB 422 DGSQIVTILSKNGASGDSYTLISLGSAGYTAGOQLTEVIGCTTVTVGSGNVVPVMAGGLP 481
QY 481 RVLYPEKLAGSKIC 495
DB 482 RVLYPEKLAGSKIC 496

RESULT 8
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match          95.8%; Score 2572; DB 14; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
```

Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
|||||
Db 1 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
|||||

QY 81 WITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLWVDVVA 140
|||||
Db 61 WITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLWVDVVA 120
|||||

QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
|||||
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
|||||

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
|||||
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
|||||

QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGT FVENHNDPR 320
|||||
Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGT FVENHNDPR 300
|||||

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
|||||
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360
|||||

QY 381 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
|||||
Db 361 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
|||||

QY 441 LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
|||||
Db 421 LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
|||||

RESULT 9
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication NO. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 95.8%; Score 2572; DB 14; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
|||||

Db 1 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
|||||

QY 81 WITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLWVDVVA 140
|||||

Db 61 WITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLWVDVVA 120
|||||

QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
|||||

Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
|||||

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
|||||

Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
|||||

QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGT FVENHNDPR 320
|||||

Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDLLYNMINTVKS DCPDSTLLGT FVENHNDPR 300
|||||

QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
|||||

Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360
|||||

QY 381 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
|||||

Db 361 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
|||||

QY 441 LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
|||||

Db 421 LSLSGAGYTAGQQLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
|||||

RESULT 10
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match 95.8%; Score 2572; DB 15; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
|||||

Db 1 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
|||||

QY 81 WITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLWVDVVA 140
|||||

Db 61 WITPVTQAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL KALSSALHERGMYLWVDVVA 120
|||||

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Qy 141 NHMGYDAGSSVDYSVFKPSSQDYFHPFCFIONYEDQTOVEDCWLGDNVTVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYSVFKPSSQDYFHPFCFIONYEDQTOVEDCWLGDNVTVSLPDLDTTK 180
Qy 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
Qy 261 PYQVMDGVLNYPYIYPLLNAPKSTSGMDDLNNINTVKSDDPDLTLLGTFVENHNDNPR 320
Db 241 PYQVMDGVLNYPYIYPLLNAPKSTSGMDDLNNINTVKSDDPDLTLLGTFVENHNDNPR 300
Qy 321 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
Qy 381 LIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 420
Qy 441 LSLSGAGYTAGOOLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGOOLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
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RESULT 11

```
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; Bisgard-Frantzen, Henrik
; Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10
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Query Match 95.8%; Score 2572; DB 17; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;

```
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 21 ATPADWRSQSIYFLLTDRFARTDGTATCATADQKYCGGTWQGIIDKLDYIQMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGTATCATADQKYCGGTWQGIIDKLDYIQMGFTAI 60
Qy 81 WITPVTQALPQTAYGDAYHGYWQDDIYSLNENYGTADDLKAALSSALHERGMVLMVDVVA 140
Db 61 WITPVTQALPQTAYGDAYHGYWQDDIYSLNENYGTADDLKAALSSALHERGMVLMVDVVA 120
Qy 141 NHMGYDAGSSVDYSVFKPSSQDYFHPFCFIONYEDQTOVEDCWLGDNVTVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYSVFKPSSQDYFHPFCFIONYEDQTOVEDCWLGDNVTVSLPDLDTTK 180
Qy 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
Qy 261 PYQVMDGVLNYPYIYPLLNAPKSTSGMDDLNNINTVKSDDPDLTLLGTFVENHNDNPR 320
Db 241 PYQVMDGVLNYPYIYPLLNAPKSTSGMDDLNNINTVKSDDPDLTLLGTFVENHNDNPR 300
Qy 321 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPYIYAGQEQHYAGGNDPANREATWLSGYPTDSELYK 360
Qy 381 LIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIIVTILSNKGASGDSYT 420
Qy 441 LSLSGAGYTAGOOLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGOOLTEVIGCTTTVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS 478
```

RESULT 12

```
US-10-980-759-7
; Sequence 7, Application US/10980759
; Publication No. US20050118695A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/980,759
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-980-759-7
```

Query Match 95.8%; Score 2572; DB 17; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;

Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 ATPADWRSQSIYFLLTDRFARTDGTATCATADQKYCGGTWQGIIDKLDYIQMGFTAI 80

Db 1 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
QY 141 NHMGYDGAGSSVDYSVFKEPSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFKEPSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVNLNPIIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLNPIIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 13

US-11-064-196-10
; Sequence 10, Application US/11064196
; Publication No. US20050170487A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/11/064,196
; PRIORITY FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-11-064-196-10

Query Match 95.8%; Score 2572; DB 20; Length 478;
Best Local Similarity 99.8%; Pred. No. 4.7e-204;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
QY 141 NHMGYDGAGSSVDYSVFKEPSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFKEPSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260

Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVNLNPIIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLNPIIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 440
Db 361 LIASANAIRNYAISKDTGFVTYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT 420
QY 441 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 498
Db 421 LSLSGAGYTAGQOLTEVIGCTTIVTSGDGNVVPVPMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 14

US-10-877-849-43
; Sequence 43, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

Query Match 95.8%; Score 2570; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 6.9e-204;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
QY 141 NHMGYDGAGSSVDYSVFKEPSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFKEPSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVNLNPIIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 320
Db 241 PYQNVMDGVNLNPIIYPLLNAPKSTSGMDDLNNMINTVKSDCPDSTLLGTFFVENHDNPR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360

Qy 381 LIASANAIRNYAISKDTGFTVYKKNPIYKDDTTIAMRKGTGSGQIVTILSNKGASGDSYT 440
Db |||||
361 LIASANAIRNYAISKDTGFTVYKKNPIYKDDTTIAMRKGTGSGQIVTILSNKGASGDSYT 420
Qy 441 LSLGAGYTAGQQLTEVIGCTTGTGSDGNVPPVMAGGLPRVLYPTEKLAGSKICS 496
Db |||||
421 LSLGAGYTAGQQLTEVIGCTTGTGSDGNVPPVMAGGLPRVLYPTEKLAGSKICS 476

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PaatSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 95.7%; Score 2569; DB 14; Length 1095;
Best Local Similarity 99.8%; Pred. No. 2.7e-203;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 21 ATPADWRQSISYFLLTDRFARTDGTTCNTADOKYCGGTWQGIIDKLDYIQMGFTAI 80
Db |||||
1 ATPADWRQSISYFLLTDRFARTDGTTCNTADOKYCGGTWQGIIDKLDYIQMGFTAI 60
Qy 81 WITPVTALPQTAYGDAYHYWQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 140
Db |||||
61 WITPVTALPQTAYGDAYHYWQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVA 120
Qy 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTVEDDCWLGDNVTSPLDITTK 200
Db |||||
121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTVEDDCWLGDNVTSPLDITTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db |||||
181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
Qy 261 PYQNYMDGVLYNPIYYPLLNAPFKSTGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 320
Db |||||
241 PYQNYMDGVLYNPIYYPLLNAPFKSTGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDPR 300
Qy 321 FASYTNDIALAKNVAAPILNDGIPIIYAGQBQHYAGGNDPANREATWLSGYPTDSSELYK 380
Db |||||
301 FASYTNDIALAKNVAAPILNDGIPIIYAGQBQHYAGGNDPANREATWLSGYPTDSSELYK 360
Qy 381 LIASANAIRNYAISKDTGFTVYKKNPIYKDDTTIAMRKGTGSGQIVTILSNKGASGDSYT 440
Db |||||
361 LIASANAIRNYAISKDTGFTVYKKNPIYKDDTTIAMRKGTGSGQIVTILSNKGASGDSYT 420
Qy 441 LSLGAGYTAGQQLTEVIGCTTGTGSDGNVPPVMAGGLPRVLYPTEKLAGSKICSSS 498
Db |||||
421 LSLGAGYTAGQQLTEVIGCTTGTGSDGNVPPVMAGGLPRVLYPTEKLAGSKICSSS 478

Search completed: November 7, 2005, 18:45:02
Job time : 274.151 secs

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing
A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: JS0240
A;Molecule type: DNA
A;Residues: 1-499 <GEN>
A;Genetics: AMY2
A;Note: the authors refer to this as isozyme II
R;Isemura, S.; Ikenaka, T.
J. Biochem. 74, 1-10, 1973
A;Reference number: A91330; MUID:74001521; PMID:4733850
A;Accession: A91330
A;Molecule type: protein
A;Residues: 206-225 <ISE>
R;Narita, K.
Proc. Jpn. Acad. 51, 285-290, 1975
A;Reference number: A93767
A;Accession: A93767
A;Molecule type: protein
A;Residues: 434-443,446-447,'Q',449-458,'GTTV',459-464,467-468,'B',470,'B',472-499 <NAR>
R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
submitted to the Brookhaven Protein Data Bank, August 1992
A;Reference number: A51548; PDB:6TAA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics: <AMY1>
A;Gene: amy1
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Genetics: <AMY2>
A;Gene: amy2; AmyII
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polys
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase 1 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 78; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
|||||
Db 99 AYHGYWQDIYSL 111
|||||

RESULT 3
ALAS3
alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N;Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S04549; A33215; A44713
R;Wiesel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c
A;Reference number: S04548; MUID:89237897; PMID:2785629
A;Accession: S04549
A;Molecule type: DNA
A;Residues: 1-499 <WIR>
A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295923

A;Accession: A33215
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-499 <WIR>
A;Cross-references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin
A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: A44713
A;Molecule type: DNA
A;Residues: 1-499 <GEN>
A;Note: the authors refer to this as isozyme I
R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics:
A;Gene: amy3; AmyI
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; meta
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase 3 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 78; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
|||||
Db 99 AYHGYWQDIYSL 111
|||||

RESULT 4
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C;Species: Aspergillus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C;Accession: JS0663
R;Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shirousami and its expressio
A;Reference number: JS0663; MUID:92323146; PMID:1368777
A;Accession: JS0663
A;Molecule type: mRNA
A;Residues: 1-499 <SHI>
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <ALP>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
|||||

Db 99 AYHGYWQDIYSL 111

RESULT 5
JT0466
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N:Alternate names: glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: JT0466
R:Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A:Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus oryzae
A:Reference number: JT0466
A:Accession: JT0466
A:Molecule type: DNA
A:Residues: 1-499 <TAD>
A:Cross-references: UNIPROT:P10529
C:Comment: See also PIR:JK0201 and PIR:JS0240.
C:Comment: One atom of calcium per molecule is essential for activity.
C:Genetics:
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: signal sequence #status predicted <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:231,251,318/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 99 AYHGYWQDIYSL 111

RESULT 6
JN0588
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N:Alternate names: Taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: JN0588
R:Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kirita, N.; Tauboi, A.; Udaoka, S.
Gene 84, 319-327, 1989
A:Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for multiple forms of the gene
A:Reference number: JN0588; MUID:90128276; PMID:2612911
A:Accession: JN0588
A:Molecule type: mRNA
A:Residues: 1-499 <TSU>
A:Cross-references: UNIPROT:Q96TH4
C:Comment: The alpha amylases are encoded by multigene family.
C:Genetics:
A:Gene: Taa-G1
A:Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: signal sequence #status predicted <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 99 AYHGYWQDIYSL 111

RESULT 8
T38770
alpha-amylase a precursor - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38770
R:Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21751
A:Accession: T38770
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-513 <SKE>
A:Cross-references: UNIPROT:O14154; EMBL:Z98762; PIDN:CAB11471.1; GSPDB:GN00066; SPDB:S72270
A:Experimental source: strain 972h-; cosmid c4A8
C:Genetics:
A:Gene: SPDB:SPAC4A8.01
A:Map position: 1
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 85.9%; Score 67; DB 2; Length 513;
Best Local Similarity 76.9%; Pred. No. 0.0027;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 100 AYHGYWQDIYSL 112

RESULT 9
S72270
alpha-amylase (EC 3.2.1.1) precursor - Cryptococcus sp. (strain CS2)
C:Species: Cryptococcus sp.
A:Variety: strain CS2
C:Date: 23-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 99 AYHGYWQDIYSL 111

RESULT 7
B48305
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: B48305
R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.
Curr. Genet. 17, 203-212, 1990
A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus awamori
A:Reference number: A48305; MUID:90254827; PMID:2340591
A:Accession: B48305
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499 <KOR>
A:Cross-references: UNIPROT:Q02906
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
Db 99 AYHGYWQDIYSL 111

A:Residues: 1-507 <CLA>
A:Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:G396561; PIDN:CAA51912.1; PID:G3961
C:Genetics:
A:Gene: SWA2
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-20/Domains: signal sequence #status predicted <SIG>
F:21-507/Product: alpha-amylase #status predicted <MAT>
F:205-332/Domains: alpha-amylase core homology <AMY>
F:134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	82.1%;	Score 64;	DB 2;	Length 507;
Best Local Similarity	69.2%;	Pred. No. 0.0084;		
Matches	9;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
110 AYHGYWMDIYAI 122
|||||:||||

Db 110 AYHGYWMDIYAI 122

RESULT 12
JK0201
alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
N:Alternate names: glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: JK0201
R:Toda, H.; Kondo, K.; Narita, K.
Proc. Jpn. Acad. 58B, 208-212, 1982
A:Title: The complete amino acid sequence of Taka-amylase A.
A:Reference number: JK0201
A:Accession: JK0201
A:Molecule type: protein
A:Residues: 1-478 <TOD>
A:Cross-references: UNIPROT:P10529
C:Comment: One atom of calcium per molecule is essential for the activity.
C:Comment: This enzyme is a glycoprotein.
C:Comment: See also PIR:JT0466 and PIR:JS0240.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domains: alpha-amylase core homology <AMY>
F:197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:210,230,297/Active site: His, Glu, Asp #status experimental

Query Match	79.5%;	Score 62;	DB 2;	Length 478;
Best Local Similarity	84.6%;	Pred. No. 0.017;		
Matches	11;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
78 AYHGYWQDIYSL 90
|||||:||||

Db 78 AYHGYWQDIYSL 90

RESULT 13
JC4510
pullulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)
N:Alternate names: LKAI protein; raw starch-degrading amylase
N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C:Species: Lipomyces kononenkoae
C:Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4510; PC4116
R:Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lip
A:Reference number: JC4510; MUID:96105202; PMID:8529855
A:Accession: JC4510
A:Molecule type: mRNA

A;Residues: 1-624 <STE>
A;Cross-references: UNIPROT:Q01117; GB:U030376; NID:g1173536; PIDN:AAC49622.1; PID:g11735
A;Experimental source: strain IGC4052B
A;Accession: PC4116
A;Molecule type: protein
A;Residues: 29-44 <ST2>
A;Experimental source: IGC4052B
C;Genetics:
A;Gene: LKAL
C;Function:
A;Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
A;Pathway: glycogen/starch degradation
C;Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-624/Product: alpha-amylase #status predicted <MAT>
F;48-141/Domain: glucoamylase starch-binding domain homology <SBD>
F;320-447/Domain: alpha-amylase core homology <AMY>
F;177-185-297-311,387-430,587-622/Disulfide bonds: #status predicted
F;304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 79.5%; Score 62; DB 1; Length 624;
Best Local Similarity 69.2%; Pred. No. 0.022;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
||||| :|||
Db 225 AYHGYWKMDFAL 237

RESULT 14
S31478
alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C;Species: Thermoactinomyces vulgaris
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S31478
R;Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; H
submitted to the EMBL Data Library, December 1992
A;Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A;Reference number: S31478
A;Accession: S31478
A;Molecule type: DNA
A;Residues: 1-482 <HOF>
A;Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g48290
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;194-319/Domain: alpha-amylase core homology <AMY>

Query Match 75.6%; Score 59; DB 2; Length 482;
Best Local Similarity 69.2%; Pred. No. 0.053;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
||||| :|||
Db 107 AYHGYWTFYSV 119

RESULT 15
ALBYAF
alpha-amylase (EC 3.2.1.1) precursor - yeast (Saccharomycopsis fibuligera)
C;Species: Saccharomycopsis fibuligera
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S00064
R;Itoch, T.; Yamashita, I.; Fukui, S.
FEBS Lett. 219, 339-342, 1987
A;Title: Nucleotide sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomycop
A;Reference number: S00064; MUID:87276512; PMID:3497057
A;Accession: S00064
A;Molecule type: DNA

A;Residues: 1-494 <ITO>
A;Cross-references: UNIPROT:P21567; EMBL:X05791; NID:g4847; PIDN:CAA29233.1; PID:g4848
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Th
C;Genetics:
A;Gene: ALP1
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metal
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-494/Product: alpha-amylase #status predicted <MAT>
F;200-327/Domain: alpha-amylase core homology <AMY>
F;57-65,177-191,267-310,462-493/Disulfide bonds: #status predicted
F;148,189,202,237/Binding site: calcium (Asn, Gln, Asp, His) #status predicted
F;224/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;233,257,324/Active site: Asp, Glu, Asp #status predicted

Query Match 74.4%; Score 58; DB 1; Length 494;
Best Local Similarity 61.5%; Pred. No. 0.079;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
||||| :|||
Db 105 AYHGYWKNYKI 117

Search completed: November 7, 2005, 18:58:45
Job time : 1.50579 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:24:00 ; Search time 6.97683 Seconds
(without alignments)
954.162 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 78
Sequence: 1 AYHGYWQDIYSL 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	498	1 AMYA ASPAW	Q02905 aspergillus
2	78	100.0	498	2 Q76CT3	Q76ct3 aspergillus
3	78	100.0	499	1 AMYA ASPOR	P10529 aspergillus
4	78	100.0	499	1 AMYA ASPAW	Q02906 aspergillus
5	78	100.0	499	1 AMY ASPSH	P30292 aspergillus
6	78	100.0	499	2 Q96TH4	Q36th4 aspergillus
7	78	100.0	499	2 Q76L39	Q76l39 aspergillus
8	78	100.0	499	2 Q7LV45	Q7lv45 aspergillus
9	75	96.2	490	2 Q9UV07	Q9uv07 emericella
10	68	87.2	128	2 Q15751	O15751 dictyosteli
11	67	85.9	513	1 AMY3 SCHPO	O14154 schizosacch
12	66	84.6	631	2 Q92334	Q92394 cryptococcu
13	64	82.1	484	1 AMYA ASPNG	P56271 aspergillus
14	64	82.1	507	1 AMY2 DEBEC	Q08806 debaryomyce
15	64	82.1	634	2 Q76L36	Q76l36 aspergillus
16	63	80.8	640	2 Q13296	O13296 aspergillus
17	62	79.5	624	1 AMY1 LIPKO	Q01117 lipomyces k
18	62	79.5	647	2 Q6YF33	Q6yf33 lipomyces s
19	59	75.6	482	2 Q60051	Q60051 thermoactin
20	59	75.6	492	2 Q7SDU6	Q7sdj6 neurospora
21	58	74.4	494	1 AMY1 SAGFI	P21567 saccharomyc
22	56	71.8	478	1 YQ29 SCHPO	O10427 schizosacch
23	54	69.2	491	2 Q13956	O13996 schizosacch
24	54	69.2	623	2 Q9UV09	Q9uv09 emericella
25	53	67.9	564	1 AMY4 SCHPO	Q9y789 schizosacch
26	52	66.7	533	2 Q7S4X0	Q7s4k0 neurospora
27	52	66.7	581	1 AMY1 SCHPO	Q09840 schizosacch
28	52	66.7	711	2 Q992E3	Q992b3 streptococc
29	50	64.1	499	2 Q8J1B4	O8j1e4 lipomyces k
30	50	64.1	512	1 AMY1 DEBEC	P19269 debaryomyce
31	50	64.1	625	2 Q74922	O74922 schizosacch

32 49 62.8 528 1 AMY_BACCI P08137 bacillus ci
33 49 62.8 686 2 Q87FR2 Q87fr2 vibrio para
34 49 62.8 687 2 Q7MCL0 Q7mcl0 vibrio vuln
35 49 62.8 687 2 Q8DSL1 Q8dsl1 vibrio vuln
36 49 62.8 690 2 Q9KL86 Q9kl86 vibrio chol
37 49 62.8 712 1 CDGT_BACS3 P09121 bacillus sp
38 49 62.8 712 2 Q6S3E3 Q6se33 bacillus sp
39 49 62.8 713 1 CDG2_PAEMA P31835 paenibacill
40 49 62.8 713 1 CDGT_BAC11 P30921 bacillus sp
41 49 62.8 713 1 CDGT_BACSO P05618 bacillus sp
42 49 62.8 713 1 CDGT_BACS8 P17692 bacillus sp
43 49 62.8 713 1 CDGU_BACCI P43379 bacillus ci
44 49 62.8 713 2 Q9F5W3 Q9f5w3 bacillus ci
45 49 62.8 718 1 CDGT_BACCI P30920 bacillus ci

ALIGNMENTS

RESULT 1
ID AMYA ASPAW STANDARD; PRT; 498 AA.
AC Q02905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase A).
GN Name=AMYA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RA "Cloning, characterization, and expression of two alpha-amylase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212(1990).
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X52755; CAA36966.1; -;
CC PIR; A48305; A48305.
CC HSP; P10529; 7TAA.
CC InterPro; IPR006589; Alp_aml_cat_sub.
CC InterPro; IPR006047; Alpha_aml_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
CC Hydroxylase; Multigene family; Signal.
CC SIGNAL 1 21 Potential.
CC CHAIN 22 498 Alpha-amylase A.
CC ACT_SITE 227 227 Nucleophile (By similarity).
CC FT ACT_SITE 251 251 Proton donor (By similarity).
CC FT ACT_SITE 318 318 By similarity.
CC FT METAL 142 142 Calcium 1 (By similarity).

```

FT METAL      183      183      Calcium 1 (via carbonyl oxygen) (By
FT METAL      196      196      similarity)
FT METAL      227      227      Calcium 1 (By similarity)
FT METAL      231      231      Calcium 1 (via carbonyl oxygen) (By
FT METAL      251      251      similarity)
FT METAL      51       59       Calcium 2 (By similarity)
FT DISULFID   171      185       By similarity
FT DISULFID   261      304       By similarity
FT DISULFID   461      496       By similarity
FT CARBOHYD   218      218       N-linked (GlcNAc...) (Potential)
SQ SEQUENCE   498 AA; 54880 MW; 7658511BC01A8A01 CRC64;
Query Match      100.0%; Score 78; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYYQDDIYSL 13
|||||
Db 99 AYHGYYQDDIYSL 111

RESULT 2
Q76CT3 PRELIMINARY; PRT; 498 AA.
ID Q76CT3
AC Q76CT3; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase.
GN Name:amyA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito K.;
CC Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB109452; BAD01051.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy1; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;
Query Match      100.0%; Score 78; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYYQDDIYSL 13
|||||
Db 98 AYHGYYQDDIYSL 110

RESULT 3
AMYA_ASPOR STANDARD; PRT; 499 AA.
ID AMYA_ASPOR
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
DE Alpha-D-glucan glucanohydrolase).
GN Name:AMY1;
GN and
GN Name:AMY2;

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GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RX MEDLINE=89237897; PubMed=2785629;
RA Wirsel S., Lachmund A., Wildhardt G., Rutkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RT Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kiritani N., Tauboi A., Uda S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";
RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzozowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.

```


Royce T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
 "Cloning, characterization, and expression of two alpha-amylase genes
 from *Aspergillus niger* var. *awamori*.";
 Curr. Genet. 17:203-212(1990).
 -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides
 -|- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 at high concentrations (By similarity).
 -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.

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 or send an email to license@isb-sib.ch).

 EMBL; X52756; CAA36967.1; -.
 F1R; B48305; B48305.
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Multigene family; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 499 Alpha-amylase B.
 FT ACT_SITE 227 227 Nucleophile (By similarity).
 FT ACT_SITE 251 251 Proton donor (By similarity).
 FT ACT_SITE 318 318 By similarity.
 FT ACT_SITE 318 318 By similarity.
 FT METAL 142 142 Calcium 1 (By similarity).
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 499 AA; 54921 MW; 740B96B11BC01A8A CRC64;
 Query Match 100.0%; Score 78; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AYHGYWQDIYSL 13
 |||||
 DB 99 AYHGYWQDIYSL 111
 RESULT 5
 AMY_ASPSH STANDARD; PRT; 499 AA.
 AC P30292;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 Glucanohydrolase).
 DE Name=AMY;
 GN *Aspergillus shirousami*.
 OS *Aspergillus shirousami*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5070;
 RN [1]

SEQUENCE FROM N.A.
 MEDLINE=92323146; PubMed=1358777;
 RX Shibuya I., Tamura G., Ishikawa T., Hara S.;
 "Cloning of the alpha-amylase cDNA of *Aspergillus shirousami* and its
 expression in *Saccharomyces cerevisiae*.";
 RT Biosci. Biotechnol. Biochem. 56:174-179(1992).
 RL -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides
 -|- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 at high concentrations (By similarity).
 -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.

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 or send an email to license@isb-sib.ch).

 EMBL; D10461; BAA01255.1; -.
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Signal.
 FT SIGNAL 1 21 Alpha-amylase.
 FT CHAIN 22 499 Nucleophile (By similarity).
 FT ACT_SITE 227 227 Proton donor (By similarity).
 FT ACT_SITE 251 251 By similarity.
 FT ACT_SITE 318 318 By similarity.
 FT METAL 142 142 Calcium 1 (By similarity).
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;
 Query Match 100.0%; Score 78; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AYHGYWQDIYSL 13
 |||||
 DB 99 AYHGYWQDIYSL 111
 RESULT 6
 Q96TH4 PRELIMINARY; PRT; 499 AA.
 ID Q96TH4
 AC Q96TH4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Taka-amylase A (EC 3.2.1.1).
 DE Name=amyA;
 GN *Aspergillus oryzae*.
 OS *Aspergillus oryzae*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5062;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=RIB40;
RX MEDLINE=20289310; PubMed=10830498;
RA Gomi K., Akeno T., Minecoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
RT gene, amyR, involved in the amylolytic gene expression in Aspergillus
RT oryzae.";
RL Biosci. Biotechnol. Biochem. 64:816-827(2000).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB021876; BAA95703.1; -.
DR FIR; JN0588; JN0588.
DR PIR; S04549; ALA53.
DR HSSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR GlycoSIDase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||
99 AYHGYYQDDIYSL 111

RESULT 7
Q76L99 PRELIMINARY; PRT; 499 AA.
AC Q76L99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Alpha-amylase precursor.
GN Name=amyl I;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB083159; BAD06002.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SIGNAL.
FT SIGNAL.
SQ SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||
99 AYHGYYQDDIYSL 111

RESULT 8
Q7LV45 PRELIMINARY; PRT; 499 AA.
AC Q7LV45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Alpha-amylase (EC 3.2.1.1).
GN Name=amyl;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5059;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-10D;
RA Fakhoury A.M., Woloshuk C.P.;
RT "Amyl, the alpha-amylase gene of Aspergillus flavus: Involvement in
RT aflatoxin biosynthesis in maize kernels.";
RL Phytopathology 89:908-914(1999).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF139525; AAF14264.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR GlycoSIDase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db |||||
99 AYHGYYQDDIYSL 111

RESULT 9
Q9UV07 PRELIMINARY; PRT; 490 AA.
AC Q9UV07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Alpha-amylase AmyA.
GN Name=amyA;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RA Boase N.A., Murphy R.M., Kelly J.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF208225; AAF17103.1; -.
DR HSSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.

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FT DISULFID 454 488      BY similarity.
FT CARBOHYD 162 162      N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 357 357      N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 513 AA; 58715 MW; 455DD97FA428C182 CRC64;

Query Match      85.9%; Score 67; DB 1; Length 513;
Best Local Similarity 76.9%; Pred. No. 0.012;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYHGWOQDIYSL 13
Db 100 AYHGYPQDLXYTL 112

RESULT 12
Q92394 PRELIMINARY; PRT; 631 AA.
AC Q92394;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
GN Name=amy-CS2;
OS Cryptococcus sp. S-2.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellomycetidae incertae sedis; Cryptococcus.
OX NCBI_TaxID=87049;
RN SEQUENCE FROM N.A.
RP STRAIN=S-2;
RX MEDLINE=96433120; PubMed=88361148;
RA Iefuji H., Chino M., Kato M., Iimura Y.;
RT "Raw-starch-digesting and thermostable alpha-amylase from the yeast
RT Cryptococcus sp. S-2: purification, characterization, cloning, and
RT sequencing.";
RL Biochem. J. 318:989-996(1996).
DR EMBL; D83541; BAA12011.1; -
DR EMBL; D83540; BAA12010.1; -
DR PIR; S72270; S72270.
DR HSSP; P10529; 7TAA.
DR GO; GO:004556; F:alpha-amylase activity; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
DR SIGNAL.
FT CHAIN 1 20
FT SIGNAL 21 631 alpha-amylase.
SQ SEQUENCE 631 AA; 67658 MW; 8196B7B6E1D707E5 CRC64;

Query Match      84.6%; Score 66; DB 2; Length 631;
Best Local Similarity 76.9%; Pred. No. 0.022;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGWOQDIYSL 13
Db 105 AYHGYPQDLXYTL 117

RESULT 13
AMYA ASPNG STANDARD; PRT; 484 AA.
AC P56271;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;

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RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=91002514; PubMed=2207069;
RA Boel E., Brady L., Brzozowski A.M., Derewenda Z., Dodson G.G.,
RA Jensen V.J., Petersen S.B., Swift H., Thim L., Woldike H.P.;
RT "Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-
RT A resolution of two enzymes from Aspergillus.";
RL Biochemistry 29:6244-6249(1990).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
DR PDB; 2AAA; X-ray; @=1-484.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; Alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW 3D-structure; Calcium-binding; Carbohydrate metabolism; Glycoprotein;
KW Glycosidase; Hydrolase.
FT ACT_SITE 206 206 Nucleophile.
FT ACT_SITE 230 230 Proton donor.
FT ACT_SITE 297 297
FT METAL 121 121 Calcium 1.
FT METAL 162 162 Calcium 1 (via carbonyl oxygen).
FT METAL 175 175 Calcium 1.
FT METAL 206 206 Calcium 2.
FT METAL 210 210 Calcium 1 (via carbonyl oxygen).
FT METAL 230 230 Calcium 2.
FT DISULFID 30 38
FT DISULFID 150 164
FT DISULFID 240 283
FT DISULFID 440 475
FT CARBOHYD 24 24 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 157 157 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 197 197 N-linked (GlcNAc... ) (Potential).
FT HELIX 3 6
FT TURN 7 8
FT STRAND 11 13
FT HELIX 16 19
FT TURN 22 23
FT HELIX 32 34
FT HELIX 42 47
FT TURN 48 48
FT HELIX 49 53
FT TURN 54 56
FT TURN 59 62
FT STRAND 66 68
FT STRAND 73 73
FT TURN 74 75
FT STRAND 76 76
FT TURN 79 80
FT STRAND 84 90
FT TURN 92 94
FT HELIX 97 108
FT TURN 109 111
FT STRAND 113 118
FT STRAND 122 122
FT STRAND 125 125
FT HELIX 129 131
FT HELIX 134 136
FT STRAND 138 138
FT HELIX 143 145
FT STRAND 146 146
FT STRAND 151 151
FT TURN 155 156
FT HELIX 158 163
FT STRAND 165 167
FT STRAND 172 173
FT STRAND 175 176
FT TURN 178 179
FT HELIX 181 198

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FT TURN 199 205
FT STRAND 202 205
FT TURN 209 210
FT HELIX 213 215
FT HELIX 216 223
FT TURN 224 224
FT STRAND 226 229
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FT HELIX 240 244
FT TURN 245 245
FT STRAND 248 250
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FT STRAND 405 410
FT TURN 414 415
FT STRAND 419 423
FT TURN 430 431
FT STRAND 433 436
FT TURN 437 440
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FT STRAND 451 455
FT TURN 457 458
FT STRAND 461 465
FT HELIX 466 469
FT TURN 470 471
FT TURN 474 475
SQ SEQUENCE 484 AA; 52935 MW; 04D596E34680656D CRC64;

Query Match 82.1%; Score 64; DB 1; Length 484;
Best Local Similarity 76.9%; Pred. No. 0.035; 2; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYDV 90

RESULT 14
AMY2 DEBOC STANDARD; PRT; 507 AA.
AC Q08806; 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase 2).
GN Name=SWA2;
OS Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OC NCBI_TaxID=27300;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 26077 / CBS 2863;
RX MEDLINE=93365041; PubMed=8358835;
RA Claros M.G., Abarca D., Fernandez-Lobato M., Jimenez A.;
RT "Molecular structure of the SWA2 gene encoding an AMY1-related alpha-
RT amylase from Schwanniomyces occidentalis.";
RL Curr. Genet. 24:75-83(1993).
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -|- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X73497; CAAS1912.1; -.
CC FIR; S33921; S33921.
CC HSP; P10529; 7TAA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Signal.
FT SIGNAL 1 20
FT CHAIN 21 507
FT ACT_SITE 238 238
FT ACT_SITE 262 262
FT ACT_SITE 329 329
FT METAL 153 153
FT METAL 194 194
FT METAL 207 207
FT METAL 238 238
FT METAL 242 242
FT METAL 262 262
FT DISULFID 62 70
FT DISULFID 182 196
FT DISULFID 272 315
FT DISULFID 470 505
FT CARBOHYD 229 229
SQ SEQUENCE 507 AA; 55966 MW; 3A562E95BD8AD63 CRC64;

Query Match 82.1%; Score 64; DB 1; Length 507;
Best Local Similarity 69.2%; Pred. No. 0.037; 3; Mismatches 1; Indels 0; Gaps 0;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 110 AYHGYWQDIYAI 122

RESULT 15
Q76L96 PRELIMINARY; PRT; 634 AA.
ID Q76L96;
AC Q76L96; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
DE Name=amy1 III;
GN Aspergillus awamori.
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Aspergillaceae; Aspergillus.
OC NCBI_TaxID=105351;
OX NCBI_TaxID=105351;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083162; BAD06005.1; -.
DR EMBL; AB083160; BAD06003.1; -.
DR HSSP; P04064; 1ACZ.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
DR SMART; SM00642; Aamy; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 1 21 Potential.
      1 21 16C0BE6AF6FB0E9B CRC64;

Query Match      82.1%; Score 64; DB 2; Length 634;
Best Local Similarity 76.9%; Pred. No. 0.047;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGTYOODIYSL 13
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Db 99 AYHGYWQQKIYDV 111

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Search completed: November 7, 2005, 18:52:30
 Job time : 7.97683 secs

The Page Book (1904)

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OM protein - protein search, using sw model

Run on: November 7, 2005, 17:47:24 ; Search time 1.95733 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 78
Sequence: 1 AYGWQDIYSL 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	478	1	US-08-720-899-7
2	78	100.0	478	1	US-08-459-610-7
3	78	100.0	478	2	US-08-343-804-7
4	78	100.0	478	2	US-08-600-908A-10
5	78	100.0	478	3	US-08-683-838A-10
6	78	100.0	478	3	US-09-182-859-7
7	78	100.0	478	4	US-09-672-459-7
8	78	100.0	478	4	US-09-636-252A-10
9	78	100.0	478	4	US-10-186-042-7
10	62	79.5	478	2	US-08-339-715A-2
11	54	69.2	468	1	US-08-204-656B-2
12	54	69.2	468	1	US-08-470-702-6
13	54	69.2	468	1	US-08-467-831-6
14	53	67.9	468	1	US-08-204-656B-4
15	53	67.9	468	1	US-08-470-702-7
16	53	67.9	468	1	US-08-467-831-7
17	50	64.1	468	1	US-08-204-656B-6
18	50	64.1	468	1	US-08-470-702-8
19	50	64.1	468	1	US-08-467-831-8
20	49	62.8	468	1	US-08-204-656B-8
21	49	62.8	468	1	US-08-470-702-9
22	49	62.8	468	1	US-08-467-831-9
23	49	62.8	685	3	US-08-947-965-72
24	49	62.8	685	3	US-08-947-965-74
25	49	62.8	686	3	US-08-947-965-70
26	49	62.8	686	3	US-08-947-965-73
27	47	60.3	624	3	US-08-947-965-78

28	47	60.3	655	1	US-08-469-202-27	Sequence 27, Appl
29	47	60.3	655	1	US-08-469-202-28	Sequence 28, Appl
30	47	60.3	655	2	US-08-484-434C-34	Sequence 34, Appl
31	47	60.3	655	2	US-08-484-434C-35	Sequence 35, Appl
32	47	60.3	655	4	US-09-384-361-34	Sequence 34, Appl
33	47	60.3	655	4	US-09-384-361-35	Sequence 35, Appl
34	46	59.0	675	3	US-08-947-965-76	Sequence 76, Appl
35	46	59.0	676	3	US-08-947-965-71	Sequence 71, Appl
36	46	59.0	680	3	US-08-947-965-77	Sequence 77, Appl
37	46	59.0	683	3	US-08-947-965-2	Sequence 2, Appl
38	46	59.0	687	3	US-08-947-965-75	Sequence 75, Appl
39	46	59.0	725	2	US-08-816-105A-1	Sequence 1, Appl
40	45	57.7	719	3	US-09-386-607-2	Sequence 2, Appl
41	45	57.7	719	4	US-09-645-707B-2	Sequence 2, Appl
42	44	56.4	14	1	US-08-204-656B-11	Sequence 11, Appl
43	44	56.4	14	1	US-08-470-702-11	Sequence 11, Appl
44	44	56.4	14	1	US-08-467-831-11	Sequence 11, Appl
45	44	56.4	454	1	US-07-930-686-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5753460o No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-720-899-7

Query Match 100.0%; Score 78; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-600-908A-10

Query Match 100.0%; Score 78; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYSL 90

RESULT 5
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: "-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-683-838A-10

Query Match 100.0%; Score 78; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYSL 90

RESULT 6
US-09-182-859-7
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; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER FILING DATE: 0515/96
; EARLIER FILING DATE: 1996-04-30
; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7

Query Match 100.0%; Score 78; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYSL 90

RESULT 7
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match 100.0%; Score 78; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
Db 78 AYHGYWQDIYSL 90
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RESULT 8
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10

Query Match 100.0%; Score 78; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||

Db 78 AYHGYWQDIYSL 90

RESULT 9
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 100.0%; Score 78; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||

Db 78 AYHGYWQDIYSL 90

RESULT 10
US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriki, Takashi
; APPLICANT: Yanase, Michio
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; TITLE OF INVENTION: NEOPULLULANASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; STREET: G. Street
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Melser, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-715A-2

Query Match 79.5%; Score 62; DB 2; Length 478;
Best Local Similarity 84.6%; Pred. No. 0.044;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
|||||

Db 78 AYHGYWQDIYSL 90

RESULT 11
US-08-204-656B-2
; Sequence 2, Application US/08204656B
; Patent No. 5538882
; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuro
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme

;; NUMBER OF SEQUENCES: 18
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
;; STREET: 8110 Gatehouse Road, Suite 500 East
;; CITY: Falls Church
;; STATE: Virginia
;; COUNTRY: U.S.A.
;; ZIP: 22042
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/204,656B
;; FILING DATE: 02-MAR-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weiner, Marc S.
;; REGISTRATION NUMBER: 32,181
;; REFERENCE/DOCKET NUMBER: 234-252P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 205-8000
;; TELEFAX: (703) 205-8050
;; TELEX: 248345
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 468 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-204-656B-2

Query Match 69.2%; Score 54; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 0.82;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGWOODIYSL 13
Db 79 AYHGFWMKNIYKI 91
|||||:|:|:|

RESULT 12
US-08-470-702-6
; Sequence 6, Application US/08470702
; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656

;; FILING DATE: 02-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEINER, MARC S.
;; REGISTRATION NUMBER: 32,181
;; REFERENCE/DOCKET NUMBER: 234-252P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 205-8000
;; TELEFAX: (703) 205-8050
;; TELEX: 248345
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 468 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; US-08-470-702-6

Query Match 69.2%; Score 54; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 0.82;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AYHGWOODIYSL 13
Db 79 AYHGFWMKNIYKI 91
|||||:|:|:|

RESULT 13
US-08-467-831-6
; Sequence 6, Application US/08467831
; Patent No. 5635378
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKUO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,831
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/204,656
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-467-831-6

Query Match 69.2%; Score 54; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 0.82; Mismatches 4; Indels 2; Gaps 0;
Matches 7; Conservative

Qy 1 AYHGWOQDIYSL 13
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Db 79 AYHGWMMKIYKI 91

RESULT 14

US-08-204-656B-4
; Sequence 4, Application US/08204656B
; Patent No. 5538882

; GENERAL INFORMATION:
; APPLICANT: Matsui, Ikuro
; APPLICANT: Ishikawa, Kazuhiko
; APPLICANT: Miyairi, Sachio
; APPLICANT: Honda, Koichi
; TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,
; TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing
; TITLE OF INVENTION: Oligosaccharide Using The Enzyme
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/204,656B
; FILING DATE: 02-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiner, Marc S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-204-656B-4

Query Match 67.9%; Score 53; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 1.2; Mismatches 4; Indels 2; Gaps 0;
Matches 7; Conservative

Qy 1 AYHGWOQDIYSL 13
|||||:|:|:
Db 79 AYHGWMMKIYKI 91

RESULT 15

US-08-470-702-7
; Sequence 7, Application US/08470702

; Patent No. 5631149
; GENERAL INFORMATION:
; APPLICANT: MATSUI, IKURO
; APPLICANT: ISHIKAWA, KAZUHIKO
; APPLICANT: MIYAIRI, SACHIO
; APPLICANT: HONDA, KOICHI
; TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
; TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
; TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,702
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/204,656
; APPLICATION NUMBER: 02-MAR-1994
; FILING DATE: 02-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 234-252P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-470-702-7

Query Match 67.9%; Score 53; DB 1; Length 468;
Best Local Similarity 53.8%; Pred. No. 1.2; Mismatches 4; Indels 2; Gaps 0;
Matches 7; Conservative

Qy 1 AYHGWOQDIYSL 13
|||||:|:|:
Db 79 AYHGWMMKIYKI 91

Search completed: November 7, 2005, 18:25:06
Job time: 1.95753 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:11:05 ; Search time 7.05212 Seconds
(without alignments)
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Title: US-10-820-200-2_COPY_98_110
Perfect score: 78
Sequence: 1 AYHGYYQDIYSL 13

Scoring table: BLOSUM62

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Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

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6: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	476	17	US-10-877-849-43
2	78	100.0	478	14	US-10-184-771-10
3	78	100.0	478	14	US-10-186-042-7
4	78	100.0	478	15	US-10-644-187-7
5	78	100.0	478	17	US-10-526-720-10
6	78	100.0	478	17	US-10-980-759-7
7	78	100.0	478	20	US-11-064-196-10
8	78	100.0	498	16	US-10-815-495-22
9	78	100.0	498	16	US-10-820-200-2
10	78	100.0	498	17	US-10-877-849-30
11	78	100.0	499	16	US-10-815-495-18
					Sequence 43, Appl
					Sequence 10, Appl
					Sequence 7, Appl
					Sequence 7, Appl
					Sequence 10, Appl
					Sequence 7, Appl
					Sequence 10, Appl
					Sequence 22, Appl
					Sequence 2, Appl
					Sequence 30, Appl
					Sequence 18, Appl

12	78	100.0	499	16	US-10-797-393A-5	Sequence 5, Appl
13	78	100.0	608	17	US-10-877-849-40	Sequence 40, Appl
14	78	100.0	640	17	US-10-877-849-36	Sequence 36, Appl
15	78	100.0	1095	14	US-10-228-063-45	Sequence 45, Appl
16	75	96.2	495	14	US-10-213-990-42	Sequence 42, Appl
17	70	89.7	494	17	US-10-486-868-13	Sequence 13, Appl
18	69	88.5	500	15	US-10-369-493-12469	Sequence 12469, A
19	67	85.9	513	15	US-10-369-493-2223	Sequence 2223, A
20	65	83.3	547	14	US-10-213-990-48	Sequence 48, Appl
21	64	82.1	484	15	US-10-416-393-1	Sequence 1, Appl
22	64	82.1	484	16	US-10-797-393A-1	Sequence 42, Appl
23	64	82.1	505	17	US-10-877-849-42	Sequence 1, Appl
24	64	82.1	511	17	US-10-877-849-8	Sequence 8, Appl
25	64	82.1	609	17	US-10-877-849-38	Sequence 38, Appl
26	64	82.1	629	17	US-10-877-849-34	Sequence 34, Appl
27	64	82.1	640	17	US-10-877-849-32	Sequence 32, Appl
28	63	80.8	555	17	US-10-877-849-15	Sequence 15, Appl
29	63	80.8	567	17	US-10-486-868-18	Sequence 18, Appl
30	63	80.8	640	17	US-10-877-007-22	Sequence 22, Appl
31	63	80.8	640	17	US-10-877-849-41	Sequence 41, Appl
32	58	74.4	630	14	US-10-213-990-45	Sequence 45, Appl
33	57	73.1	263	16	US-10-425-115-291647	Sequence 291647, A
34	57	73.1	549	17	US-10-486-868-14	Sequence 22723, A
35	56	71.8	493	15	US-10-369-493-22723	Sequence 22679, A
36	53	67.9	564	15	US-10-369-493-22679	Sequence 22, Appl
37	52	66.7	711	16	US-10-474-792-22	Sequence 44, Appl
38	49	62.8	686	17	US-10-872-198-44	Sequence 44, Appl
39	49	62.8	686	18	US-10-872-197A-44	Sequence 52, Appl
40	49	62.8	686	18	US-10-787-219A-52	Sequence 44, Appl
41	49	62.8	686	20	US-11-021-951-44	Sequence 4, Appl
42	49	62.8	713	17	US-10-504-543-4	Sequence 4, Appl
43	48	61.5	502	14	US-10-081-872-108	Sequence 108, App
44	48	61.5	502	15	US-10-385-305-108	Sequence 108, App
45	47	60.3	483	15	US-10-369-493-597	Sequence 597, App

ALIGNMENTS

RESULT 1

US-10-877-849-43

; Sequence 43, Application US/10877849

; Publication No. US20050054071A1

; GENERAL INFORMATION:

; APPLICANT: Udagawa, Hiroaki

; APPLICANT: Taira, Rikako

; APPLICANT: Tkagi, Shinobu

; APPLICANT: Allain, Eric

; APPLICANT: Hjort, Carsten

; APPLICANT: Vikso-Nielsen, Anders

; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING

; FILE REFERENCE: 10490.500-US

; CURRENT APPLICATION NUMBER: US/10/877,849

; CURRENT FILING DATE: 2004-06-25

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 43

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Aspergillus oryzae

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: (1)..(476)

US-10-877-849-43

Query Match 100.0%; Score 78; DB 17; Length 476;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYYQDIYSL 13

DB 78 AYHGYYQDIYSL 90

RESULT 2
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match 100.0%; Score 78; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDDIYSL 13
||| ||||| |||||
DB 78 AVHGYWQDDIYSL 90

RESULT 3
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 100.0%; Score 78; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDDIYSL 13
||| ||||| |||||
DB 78 AVHGYWQDDIYSL 90

RESULT 4
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match 100.0%; Score 78; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDDIYSL 13
||| ||||| |||||
DB 78 AVHGYWQDDIYSL 90

RESULT 5
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; Bisgard-Frantzen, Henrik
; Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475

REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 100.0%; Score 78; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
|||||
Db 78 AYHGYWQDDIYSL 90

RESULT 6

US-10-980-759-7
Sequence 7, Application US/10980759
Publication No. US20050118695A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/980,759
CURRENT FILING DATE: 2004-11-03
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 478
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-980-759-7

Query Match 100.0%; Score 78; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
|||||
Db 78 AYHGYWQDDIYSL 90

RESULT 7

US-11-064-196-10
Sequence 10, Application US/11064196
Publication No. US20050170487A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/11/064,196
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 478
TYPE: PRT
ORGANISM: A. oryzae
US-11-064-196-10

Query Match 100.0%; Score 78; DB 20; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
|||||
Db 78 AYHGYWQDDIYSL 90

RESULT 8

US-10-815-495-22
Sequence 22, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
TITLE OF INVENTION: Mutants Of Aspergillus Niger
FILE REFERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 498
TYPE: PRT
ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 100.0%; Score 78; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDDIYSL 13
|||||
Db 99 AYHGYWQDDIYSL 111

RESULT 9

US-10-820-200-2
Sequence 2, Application US/10820200
Publication No. US20040229764A1
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Pedersen, Sven
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
FILE REFERENCE: 5835.200-US
CURRENT APPLICATION NUMBER: US/10/820,200
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US/09/710,339
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/165,786
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2

4

; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 78; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
| | | | | | | | | | | | | | |
Db 98 AYHGYWQDIYSL 110

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lahanan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228.063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 100.0%; Score 78; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13
| | | | | | | | | | | | | | |
Db 78 AYHGYWQDIYSL 90

Search completed: November 7, 2005, 18:45:03
Job time : 8.05212 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:55 ; Search time 7.47876 Seconds
(without alignments)
672.288 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AHHGYWQDIYSL 13

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	478	2 AAR46065	Mutant al
2	13	100.0	478	2 AAR72450	Aspergill
3	13	100.0	478	2 AAR78270	Aspergill
4	13	100.0	478	2 AAW14500	Aspergill
5	13	100.0	498	4 AAB84206	Amino aci
6	13	100.0	498	8 ADT89632	Aspergill
7	13	100.0	499	8 ADT89628	Aspergill
8	13	100.0	1095	6 ABP96630	Alpha-amy
9	12	92.3	495	6 ABB80177	Aspergill
10	11	84.6	423	4 ABB09072	Aspergill
11	9	69.2	494	6 ABP97894	Amino aci
12	8	61.5	484	5 AAE24207	Aspergill
13	8	61.5	484	8 ADS75939	Aspergill
14	7	53.8	630	6 ABB80178	A. fumiga
15	6	46.2	31	2 AAR85808	Peptide r
16	6	46.2	55	2 AAR88213	Alpha-amy
17	6	46.2	429	8 ADS44209	Bacterial
18	6	46.2	468	2 AAR24136	Alpha-amy
19	6	46.2	483	8 ADN17944	Bacterial
20	6	46.2	493	2 AAR88212	Alpha-amy
21	6	46.2	493	8 ADS44293	Bacterial
22	6	46.2	494	1 AAP70571	Alpha-amy
23	6	46.2	500	8 ADS23436	Bacterial
24	6	46.2	511	1 AAP81161	Recombina
25	6	46.2	511	1 AAP81180	Sequence

26	6	46.2	512	2 AAR07574	Alpha-amy
27	6	46.2	513	8 ADN19570	Bacterial
28	6	46.2	514	2 AAW84268	Candida a
29	6	46.2	547	6 ABB80179	A. fumiga
30	6	46.2	549	6 ABP97895	Amino aci
31	6	46.2	555	6 ABP97896	Amino aci
32	6	46.2	564	8 ADS44249	Bacterial
33	6	46.2	567	6 ABP97899	Amino aci
34	6	46.2	567	2 AAR06109	Sequence
35	6	46.2	686	1 AAP61518	Sequence
36	6	46.2	686	2 AAW17605	Bacillus
37	6	46.2	686	2 AAW17600	Bacillus
38	6	46.2	686	2 AAW17603	Bacillus
39	6	46.2	686	2 AAW17592	Bacillus
40	6	46.2	686	2 AAW17596	Bacillus
41	6	46.2	686	2 AAW06773	Wild type
42	6	46.2	686	2 AAW17599	Bacillus
43	6	46.2	686	2 AAW17594	Bacillus
44	6	46.2	686	2 AAW17595	Bacillus
45	6	46.2	686	2 AAW17593	Bacillus

ALIGNMENTS

RESULT 1
AAR46065
ID AAR46065 standard; protein; 478 AA.
XX
AC AAR46065;
XX
DT 25-MAR-2003 (revised)
DT 18-JUL-1994 (first entry)
XX
DE Mutant alpha-amyase.
XX
KW Methionine substitution; stability; activity; detergent;
KW dishwashing agents; liquefaction agents.
XX
OS Aspergillus oryzae.
XX
PN WO9402597-A1.
XX
PD 03-FEB-1994.
XX
PF 06-JUL-1993; 93WO-DK000230.
XX
PR 23-JUL-1992; 92DK-00000946.
PR 16-DEC-1992; 92DK-00001503.
PR 15-MAR-1993; 93DK-00000292.
XX
(NOVO) NOVO-NORDISK AS.
XX
Svendsen A, Bisgaard-Frantzen H;
XX
WPI; 1994-048855/06.
XX
Mutant alpha-amyase from Bacillus species comprising a methionine substitution - with improved stability and activity at low pH, for use in detergents, dishwashing agents and liquefaction agents.
XX
Claim 1; Page 7; 20pp; English.
XX
The sequence os that of the Aspergillus oryzae alpha amyase, sold commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amyase exhibits a better activity level and better stability in the presence of oxidizing agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for detergents, dishwashing agents and liquefaction agents. (Updated on 25-MAR-2003 to correct PN field.)
XX

```

SQ Sequence 478 AA;
  Query Match          100.0%; Score 13; DB 2; Length 478;
  Best Local Similarity 100.0%; Pred. No. 2e-06;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 2
AAR72450
ID AAR72450 standard; protein; 478 AA.
XX AC
XX AAR72450;
XX AC
XX AAR72450;
DT 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)
XX AC
XX Aspergillus oryzae alpha amylase (mature protein).
XX AC
XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;
KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;
KW thermostable.
XX AC
XX Aspergillus oryzae.
XX OS
XX WO9510603-A1.
XX PN
XX PD
XX 20-APR-1995.
XX PF
XX 05-OCT-1994; 94WO-DK000370.
XX PR
XX 02-FEB-1994; 94DK-00000141.
XX PA (NOVO) NOVO-NORDISK AS.
XX PI Toft AH, Marcher D, Pedersen HH, Nilsson TE;
XX WPI; 1995-283767/37.
XX DR
XX Use of an oxidation stable alpha-amylase - for simultaneous desizing and
PT bleaching or scouring of fabrics contg. starch or starch derivs.
XX PS
XX Disclosure; Page 25-26; 37pp; English.
XX CC
XX Oxidation stable alpha amylases can be used for the simultaneous desizing
CC and bleaching or scouring of a fabric comprising starch or starch
CC derivatives. They exhibit a better heat stability, especially in the
CC presence of oxidising agents. They are obtained from a parent alpha
CC amylase by replacing one or more methionine residues with any amino acid
CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
CC Asp. The parent alpha amylase is pref. derived from a Bacillus species,
CC although alpha amylases of fungal origin can also be used. This sequence
CC is the wild type (unmodified) alpha amylase of Aspergillus oryzae
XX SQ Sequence 478 AA;

  Query Match          100.0%; Score 13; DB 2; Length 478;
  Best Local Similarity 100.0%; Pred. No. 2e-06;
  Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
Db 78 AYHGYWQDDIYSL 90

RESULT 4
AAW14500
ID AAW14500 standard; protein; 478 AA.
XX AC
XX AAW14500;
XX AC
XX 04-JUN-1997 (first entry)
XX DT
XX DE
XX Aspergillus oryzae alpha-amylase (mature protein).
XX AC
XX alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
KW Aspergillus oryzae; Bacillus amyloliquefaciens; altered property;
KW calcium dependency; substrate binding; stability; pH optimum;
KW thermostability; cleavage; oligosaccharide substrate; dishwashing;
KW washing; detergent additive; fabric desizing; starch liquefaction;
KW sweetener; ethanol production; variant.
XX OS
XX Aspergillus oryzae.

```


DE Amino acid sequence of a fungamyl-like alpha-amylase.
XX
KW Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
KW alcohol; starch; dough improver; brewing; starch liquification.
XX
OS Aspergillus oryzae.
XX
PN WO200134784-A1.
XX
PD 17-MAY-2001.
XX
XX 10-NOV-2000; 2000WO-DK000626.
PF
XX 10-NOV-1999; 99DK-00001617.
PR
XX (NOVO) NOVOZYMES AS.
PA
XX Bisgard-Frantzen H, Svendsen A, Pedersen S;
PI
XX WPI; 2001-367478/38.
DR
XX N-PSDB; AAF90208.
DR
XX New variant of Fungamyl-like alpha-amylase, useful for production of
PT maltose syrups, includes mutations that improve stability against heat
PT and acidic pH.
PT
XX
PS Claim 1; Page 42-45; 49pp; English.
XX
XX The present sequence represents a fungamyl-like alpha-amylase. The
CC specification describes variants of this fungamyl-like alpha-amylase,
CC which have an alteration in one the amino acid regions 98-110, 150-160,
CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
CC substitution of an amino acid or an insertion of an amino acid downstream
CC of a particular position. The variants retain alpha-amylase activity, and
CC have better heat stability and/or stability at acidic pH, relative to
CC wild-type enzyme. The variants can therefore be used at higher
CC temperatures (more efficient conversion or faster reaction, and have
CC reduced need for cooling and reduced risk of contamination). The variants
CC may also be used in conjunction with other enzymes, particularly
CC glucoamylase during dextrinisation. The variants are used to produce
CC syrups, particularly of high maltose content, or alcohol, from starch; as
CC dough improver for baked goods; in brewing, to increase fermentability of
CC the wort; and for liquefaction of starch
XX
SQ Sequence 498 AA;

Query Match 100.0%; Score 13; DB 4; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
DB 98 AYHGYWQDDIYSL 110

RESULT 6
ADT89632
ID ADT89632 standard; protein; 498 AA.
XX
XX AC ADT89632;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
XX KW Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.
XX
XX OS Aspergillus niger.
XX
XX FN US2004191864-A1.
XX
XX PD 30-SEP-2004.
XX

PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX
XX WPI; 2004-708545/69.
DR N-PSDB; ADT89631.
DR
XX
XX Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX
XX Example 11; SEQ ID NO 22; 58pp; English.
XX
XX The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
SQ Sequence 498 AA;

Query Match 100.0%; Score 13; DB 8; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDDIYSL 13
DB 99 AYHGYWQDDIYSL 111

RESULT 7
ADT89628
ID ADT89628 standard; protein; 499 AA.
XX
XX AC ADT89628;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Aspergillus niger neutral alpha-amylase B (amyB) protein.
XX
XX KW Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
XX
XX OS Aspergillus niger.
XX
XX FN US2004191864-A1.
XX
XX PD 30-SEP-2004.
XX
XX PF 31-MAR-2004; 2004US-00815495.
XX
XX PR 31-MAR-2003; 2003US-0459902P.
XX
XX PA (NOVO) NOVOZYMES BIOTECH INC.
XX
XX PI Connelly M, Brody H;
XX
XX WPI; 2004-708545/69.
DR N-PSDB; ADT89627.
DR
XX
XX Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX
XX Example 10; SEQ ID NO 18; 58pp; English.
XX
PS

XX The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase B (anyB) protein.
XX
SQ Sequence 499 AA;

Query Match 100.0%; Score 13; DB 8; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDDIYSL 13
Db 99 AVHGYWQDDIYSL 111
|||||
RESULT 8
ABP96630
ID ABP96630 standard; protein; 1095 AA.
XX
AC ABP96630;
XX
DT 02-JUN-2003 (first entry)
XX
DE Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
XX
KW Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
KW pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW maltodextrin; ethanol; fermentation; beverage; enzyme.
XX
OS Aspergillus shirousami.
XX Synthetic.
XX
PN WO2003018766-A2.
XX
PD 06-MAR-2003.
XX
PF 27-AUG-2002; 2002WO-US027129.
XX
PR 27-AUG-2001; 2001US-0315281P.
XX
PA (SYGN) SYNGENTA PARTICIPATONS AG.
XX
PI Lanahan MB, Basu SS, Batie CJ, Chen W, Craig J, Kinkema M;
XX
DR WPI; 2003-268420/26.
DR N-PSDB; ACC44572.
XX
PT Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
PT alpha-amylase, useful for producing plant to produce food products having
PT improved taste or fermentable substrates for ethanol.
XX
PS Claim 1; Page 107; 159pp; English.
XX
CC The present invention describes polynucleotides which encode processing
CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
CC isomerase, or glucoamylase) that are optimised for expression in plants.
CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
CC processing enzymes, which are activated under suitable conditions to act
CC upon the desired substrate. Also described are self-processing transgenic
CC plants and plant parts, e.g. grain, which express one or more of these
CC enzymes and have an altered composition that facilitates plant and grain
CC processing. Also described is a method (M) for converting starch to
CC starch-derived products in a transformed plant part (TPP), by activating
CC the starch processing enzyme contained in it. Transgenic grain is useful
CC for preparing maltodextrin. A transformed plant (TP) can be used to
CC produce food products having improved taste and to produce fermentable

CC substrates for ethanol and fermented beverages. (M) eliminates the need
CC to mill or physically disrupt the integrity of plant parts prior to
CC recovery of starch-derived products. The present sequence represents
CC alpha-amylase/glucoamylase fusion protein, which is given in the
CC exemplification of the present invention
XX
SQ Sequence 1095 AA;

Query Match 100.0%; Score 13; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVHGYWQDDIYSL 13
Db 78 AVHGYWQDDIYSL 90
|||||
RESULT 9
ABB80177
ID ABB80177 standard; protein; 495 AA.
XX
AC ABB80177;
XX
DT 11-AUG-2003 (first entry)
XX
DE A. fumigatus AFAAL1.
XX
KW Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KW glyceride; starch; maltodextrin; oxidated phenolic compound;
KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KW textile; tea liquor; cleaning ability.
XX
OS Aspergillus fumigatus.
XX
PN WO2003012071-A2.
XX
PD 13-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024842.
XX
PR 03-AUG-2001; 2001US-0309870P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Jiang B, Storms R, Roemer T, Bussey H;
XX
DR WPI; 2003-332729/31.
DR N-PSDB; ABQ80345, ABQ80346.
XX
PT Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.
XX
PS Claim 17; Page 134-35; 169pp; English.
XX
CC The sequences given in ABB80164-87 show enzymatic proteins derived from
CC A. fumigatus. These proteins display the catalytic activity of an enzyme
CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
CC galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for

modulating the amount of glyceride in a composition. Compositions comprising alpha-amylases are useful for modulating the amount of starches or maltodextrins in a composition. Compositions comprising laccase are useful for modulating the amount of oxidated phenolic compounds in a composition. Compositions comprising polygalacturonases are useful for modulating the amount of high or low molecular weight polygalacturonic acid chains in a composition. Compositions comprising xylanases are useful for modulating the amount of xylan or xylo-oligomers in a composition. The A. fumigatus proteins and corresponding DNA's are useful in various industries such as those involved in the making of food and feed, beverages, textiles and detergents. The DNA's are useful to express recombinant enzymes for characterization, modification or industrial uses, to compare with the nucleotide sequence of A. fumigatus to identify duplicated genes of paralogs having the same or similar biochemical activity and/or function, to compare with nucleic acid sequence of other related or distant fungal organisms to identify potential orthologous enzyme genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, and to raise anti-protein antibodies. The polypeptide having tannase activity increases the yield of tea liquor from tea leaves, improves the colour, flavour and health benefits of tea products, particularly an instant tea product. The polypeptide having cellulase activity enhances cleaning ability of detergent compositions

XX SQ Sequence 495 AA;

Query Match 92.3%; Score 12; DB 6; Length 495;
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYS 12
 |||||
 DB 97 AYHGYWQDIYS 108

RESULT 10
 ABB09072
 ID ABB09072 standard; protein; 423 AA.
 XX
 AC ABB09072;
 XX
 DT 26-JUN-2002 (first entry)
 XX
 DE Aspergillus oryzae TAKA protein (TAA).
 XX
 KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
 XX protein co-ordinate data; 3 dimensional structure.

OS Aspergillus oryzae.
 XX KR2001027418-A.
 XX
 PD 06-APR-2001.
 XX
 PF 09-SEP-1999; 99KR-00039130.
 XX
 PR 09-SEP-1999; 99KR-00039130.
 XX
 XX (POST-) POSTECH FOUND.
 PA (SAMY-) SAMYANG GENEX CORP.
 XX
 PI Kim TJ, Park GH;
 XX
 DR WPI; 2001-534477/59.
 XX
 PT Manufacturing maltogenic amylase having improved transglycosylation
 PT activity, comprises using crystallization.

PS Disclosure; Page 188; 196pp; Korean.
 XX
 CC The present invention describes manufacturing maltogenic amylase (EC
 CC 3.2.1.133) having improved transglycosylation activity, comprising using
 CC crystallisation and the three dimensional structure of maltogenic

CC amylase. Manufacturing maltogenic amylase comprises the following steps:
 CC (i) obtaining a gene of maltogenic amylase from *Thermus* sp. IM6501 (KCTC
 CC 5027BP) and inserting the gene into plasmid pUC119 to construct
 CC recombinant DNA (pTNA119); (ii) inserting the recombinant DNA to
 CC *Escherichia coli* MC1061, which is cultivated at 37 plus degrees Celsius
 CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
 CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
 CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
 CC supernatant through column chromatography and obtaining purified
 CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two
 CC maltogenic amylase molecules, and a *Thermus* sp. IM6501 maltogenic amylase
 CC (TMA) crystal. The amylase has a structure containing an activated
 CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
 CC and a pocket with glucose bound that consists of amino acid residues of
 CC Pro44, Tyr45, Arg81, Arg83, Prol18, Cys116, Asn131, Glu132, Val1329,
 CC and His1360. The present sequence represents *Aspergillus oryzae* TAKA
 CC protein (TAA), given in comparison with TMA in the present invention
 XX SQ Sequence 423 AA;

Query Match 84.6%; Score 11; DB 4; Length 423;
 Best Local Similarity 100.0%; Pred. No. 0.00029;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HGYWQDIYSL 13
 |||||
 DB 76 HGYWQDIYSL 86

RESULT 11
 ABB97894
 ID ABB97894 standard; protein; 494 AA.
 XX
 AC ABB97894;
 XX
 DT 17-JUN-2003 (first entry)
 XX
 DE Amino acid sequence of an alpha-amylase of *Aspergillus niger*.
 XX
 KW Alpha-amylase; enzyme; endohydrolysis; 1,4-alpha-glucosidic linkage;
 KW oligosaccharide; polysaccharide; baking.
 XX
 OS Aspergillus niger.
 XX
 PN WO2003016535-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 02-AUG-2002; 2002WO-NL000522.
 XX
 PR 16-AUG-2001; 2001EP-00000379.
 PR 16-AUG-2001; 2001EP-00000380.
 PR 16-AUG-2001; 2001EP-00000381.
 PR 16-AUG-2001; 2001EP-00000382.
 PR 16-AUG-2001; 2001EP-00000383.
 PR 16-AUG-2001; 2001EP-00000384.
 XX (STAM) DSM NV.

XX Maier D, Stock A, Wagner C, Folkers U, Albermann K, Hopper S;
 XX WPI; 2003-312758/30.
 XX
 DR New polynucleotide from a filamentous fungus, preferably *Aspergillus*
 PT *niger*, useful in a baking process.
 XX
 PS Claim 13; Page 61-63; 81pp; English.
 XX
 CC The present sequence is an alpha-amylase enzyme of the filamentous fungus
 CC *Aspergillus niger*. Alpha-amylases catalyse the endohydrolysis of 1,4-
 CC alpha-glucosidic linkages in oligosaccharides and polysaccharides. The
 CC alpha-amylase polynucleotides and polypeptides of the invention are
 CC useful in a baking process

```
XX SQ Sequence 494 AA;
Query Match 69.2%; Score 9; DB 6; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQD 9
    |||||
DB 94 AYHGYWQD 102

RESULT 12
ID AAE24207 standard; protein; 484 AA.
XX
AC AAE24207;
XX
DT 04-OCT-2002 (first entry)
XX
DE Aspergillus niger alpha-amylase protein.
XX
KW Ethanol production; starch; fermentation; liquefaction; alpha-amylase;
KW fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.
XX
OS Aspergillus niger.
XX
PN WO200238787-A2.
XX
PD 16-MAY-2002.
XX
PF 09-NOV-2001; 2001WO-DK000737.
XX
PR 10-NOV-2000; 2000DK-00001676.
XX
PR 21-NOV-2000; 2000US-0252213P.
XX
PR 11-DEC-2000; 2000DK-00001854.
XX
PR 15-DEC-2000; 2000US-0256015P.
XX
(PNOVO ) NOVOZYMES AS.
PA (NOVO ) NOVOZYMES NORTH AMERICA INC.
XX
PI Veit C, Felby C, Fuglsang CC;
XX
WPI; 2002-479793/51.
XX
PT Producing ethanol from starch-containing material e.g., tubers, roots,
PT whole grain, for use in fuel, by fermentation comprises carrying out a
PT secondary liquefaction step in the presence of a thermostable acid alpha-
PT amylase.
XX
PS Claim 35; Page 31-33; 33pp; English.
XX
CC The invention relates to a method for producing ethanol from starch-
CC containing material, by fermentation. The method involves carrying out a
CC secondary liquefaction step in the presence of a thermostable acid alpha-
CC amylase. The method is used in producing ethanol from a starch-containing
CC material such as tubers, roots or whole grain (e.g. corn, wheat or barley
CC or their combination) or combination of the materials. Preferably ethanol
CC is produced from starch-containing material that is obtained from cereals
CC or from corns, cobs, wheat, barley, rye, milo and potatoes or their
CC combination. The ethanol produced by above mentioned method is used as
CC fuel alcohol and/or fuel additive. The ethanol is also useful as drinking
CC ethanol i.e., potable neutral spirits or industrial ethanol. The present
CC sequence is Aspergillus niger alpha-amylase protein
XX
SQ Sequence 484 AA;
Query Match 61.5%; Score 8; DB 5; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQ 8
    |||||
DB 78 AYHGYWQ 85

RESULT 14
ABB80178
ID ABB80178 standard; protein; 630 AA.
XX
AC ABB80178;
XX
DT 11-AUG-2003 (first entry)
XX
DE A. fumigatus AFAAL2.
XX
KW Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
```

KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KW glyceride; starch; maltodextrin; oxidated phenolic compound;
KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KW textile; tea liquor; cleaning ability.

XX Aspergillus fumigatus.

OS
XX WO2003012071-A2.

PN
XX 13-FEB-2003.

PD
XX 05-AUG-2002; 2002WO-US024842.

PF
XX 03-AUG-2001; 2001US-0309870P.

PR
XX (ELIT-) ELITRA PHARM INC.

PA
XX Jiang B, Storms R, Roemer T, Bussey H;

PI
XX WPI; 2003-332729/31.

DR
XX N-PSDB; ABQ80347, ABQ80348.

XX Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.

XX Claim 17; Page 139-40; 169pp; English.

XX The sequences given in ABB80164-87 show enzymatic proteins derived from
CC A. fumigatus. These proteins display the catalytic activity of an enzyme
CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
CC galactosidases, invertase, lipase, alpha-amylase, lactase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.

CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidases are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC lactase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A.fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions

XX Sequence 630 AA;

Query Match 53.8%; Score 7; DB 6; Length 630;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YHGYWQQ 8
|||
Db 102 YHGYWQQ 108

RESULT 15

AAR85808
ID AAR85808 standard; peptide; 31 AA.

XX
AC AAR85808;

XX
DT 13-SEP-1996 (first entry)

XX Peptide rII from the WD-40 domain-contg. TUP1 protein.

XX WD40 repeat region; beta-transducin; protein-protein interaction; drug;
KW intracellular signalling; protein kinase C; homology; motif; modulator;
KW receptors of activated protein kinase; enzyme activity; isozyme; human.

XX Synthetic.

XX WO9521252-A2.

XX 10-AUG-1995.

XX 31-JAN-1995; 95WO-US001210.

XX 01-FEB-1994; 94US-00190802.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D, Ron D;

XX WPI; 1995-283772/37.

XX New WD-40 (beta-transducin)-derived polypeptide(s) - which alter the
PT activity of a protein, eg. protein kinase C, which interacts with a
PT protein contg. a WD-40 region.

XX Claim 3; Page 271; 351pp; English.

XX The peptides AAR84928-R85063 and AAR85786-R85842 are peptides derived
CC from the WD40 regions of a range of proteins (AAR85851-R85893) containing
CC WD-40 (also called beta-transducin) amino acid repeat regions. The WD-40
CC regions are involved in protein-protein interactions between proteins
CC involved in intracellular signalling. An example of such an interaction
CC is between protein kinase C and receptors of activated protein kinase
CC (RACK), esp. RACK-1 (AAR85850). The proteins were isolated based on
CC homology with beta-transducin or with its WD-40 consensus sequence. The
CC peptides can be used to identify target proteins contg. WD-40 motifs, as
CC modulators of enzyme esp. isozyme, activity of proteins involved in
CC protein-protein interaction and to screen for drugs that will affect
CC protein-protein interaction involving WD-40 domains. This peptide is
CC derived from the repeat II from the TUP1 protein

SQ Sequence 31 AA;

Query Match 46.2%; Score 6; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QDIYSL 13
|||

Db 4 QDIYSL 9
|||

Search completed: November 7, 2005, 19:27:55
Job time : 8.47876 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:15:40 ; Search time 1.58108 Seconds
(without alignments)
791.116 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AVHGYWQDIYSL 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	498	2 A48305	alpha-amylase (EC
2	13	100.0	499	1 ALAS1	alpha-amylase (EC
3	13	100.0	499	1 ALAS3	alpha-amylase (EC
4	13	100.0	499	2 JS0663	alpha-amylase (EC
5	13	100.0	499	2 JT0466	alpha-amylase (EC
6	13	100.0	499	2 JN0588	alpha-amylase (EC
7	13	100.0	499	2 B48305	alpha-amylase (EC
8	8	61.5	484	1 A35282	alpha-amylase (EC
9	6	46.2	429	2 T41560	phenylalanyl-trna
10	6	46.2	478	2 T40860	probable alpha-am
11	6	46.2	482	2 S31478	alpha-amylase (EC
12	6	46.2	483	2 G75392	glycosyl hydrolase
13	6	46.2	491	2 T38448	probable alpha-am
14	6	46.2	494	1 ALBYAF	alpha-amylase (EC
15	6	46.2	507	2 S33921	alpha-amylase (EC
16	6	46.2	512	2 S23355	alpha-amylase (EC
17	6	46.2	512	2 S06115	alpha-amylase (EC
18	6	46.2	513	2 T38770	alpha-amylase a pr
19	6	46.2	538	1 ALBSK	alpha-amylase (EC
20	6	46.2	564	2 T41503	alpha-amylase - fi
21	6	46.2	614	2 S58306	WD-40 repeat regul
22	6	46.2	624	1 JC4510	pullulanase (EC 3
23	6	46.2	625	2 T41603	alpha-amylase - fi
24	6	46.2	631	2 S72270	alpha-amylase (EC
25	6	46.2	690	2 B82409	alpha-amylase VCA0
26	6	46.2	712	1 ALBSG3	cyclomaltodextrin
27	6	46.2	713	1 ALBSG7	cyclomaltodextrin
28	6	46.2	713	1 ALBSG1	cyclomaltodextrin
29	6	46.2	713	1 ALBSXR	cyclomaltodextrin

30	6	46.2	713	2 A58800	cyclomaltodextrin
31	6	46.2	713	2 S09196	cyclomaltodextrin
32	6	46.2	713	2 JN0133	WD-40 repeat regul
33	6	46.2	718	1 ALBSG6	cyclomaltodextrin
34	6	46.2	718	1 ALBSGC	cyclomaltodextrin
35	6	46.2	718	1 ALBSMX	cyclomaltodextrin
36	5	38.5	20	2 S50175	kallikrein (PK-120
37	5	38.5	87	2 E95193	yimG protein (Impo
38	5	38.5	87	2 B99060	conserved hypotet
39	5	38.5	103	2 AF1183	hypothetical prote
40	5	38.5	103	2 AG1540	hypothetical prote
41	5	38.5	189	2 P97007	xanthine phosphori
42	5	38.5	204	2 AF1237	SOS response regul
43	5	38.5	204	2 AC1600	SOS response regul
44	5	38.5	218	2 B86801	prophage p13 prote
45	5	38.5	227	2 P96955	ABC-transporter, A

ALIGNMENTS

RESULT 1

A48305 alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori

C;Species: Aspergillus awamori

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: A48305

R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;

Curr. Genet. 17, 203-212, 1990

A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe

A;Reference number: A48305; MUID:90254827; PMID:2340591

A;Accession: A48305

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-498 <KOR>

A;Cross-references: UNIPROT:Q02905

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 13; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy' 1 AVHGYWQDIYSL 13

Db 99 AVHGYWQDIYSL 111

RESULT 2

ALAS1

alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae

N;Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A

C;Species: Aspergillus oryzae

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C;Accession: S04548; A33214; J50240; A91930; A93767; A10627

R;Wiesel, S.; Lachmund, A.; Wildhardt, G.; Rutkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon

A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Accession: S04548

A;Molecule type: DNA

A;Residues: 1-499 <WIR>

A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:G2430; PIDN:CAA31218.1; PID:G29592

A;Genetics: AMY1

A;Accession: A33214

A;Molecule type: mRNA

A;Residues: 1-499 <W12>

A;Cross-references: GB:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

A;Accession: A33215
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-499 <WT2>
A;Cross-references: GB:X12727; NID:G2454; PIDN:CAA31220.1; PID:g295922
R;Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin
A;Reference number: JS0240; MUID:89378767; PMID:2789162
A;Accession: A44713
A;Molecule type: DNA
A;Residues: 1-499 <GEN>
A;Note: the authors refer to this as isozyme I
R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A;Title: Structure and possible catalytic residues of Taka-amylase A.
A;Reference number: A37454; MUID:84212370; PMID:6609921
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics:
A;Gene: amy3; AmyI
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; meta
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase 3 #status experimental <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 13; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13
Db 99 AYHGYYQDDIYSL 111

RESULT 4
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C;Species: Aspergillus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C;Accession: JS0663
R;Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyamii and its expressio
A;Reference number: JS0663; MUID:92323146; PMID:1368777
A;Accession: JS0663
A;Molecule type: mRNA
A;Residues: 1-499 <SHI>
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <ALP>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYYQDDIYSL 13

Db 99 AYHGYWQDIYSL 111

RESULT 5

JT0466
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N;Alternate names: Glycogenase; Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: JT0466
R;Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A;Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus oryzae
A;Reference number: JT0466

A;Accession: JT0466
A;Molecule type: DNA
A;Residues: 1-499 <TAD>
A;Cross-references: UNIPROT:P10529
C;Comment: See also PIR:JK0201 and PIR:JS0240.
C;Comment: One atom of calcium per molecule is essential for activity.
C;Genetics:
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;231,251,318/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13

Db 99 AYHGYWQDIYSL 111

RESULT 6

JN0588
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N;Alternate names: Taka-amylase A
C;Species: Aspergillus oryzae
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JN0588
R;Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kiritu, N.; Tsuboi, A.; Uda, S.
Gene 84, 319-327, 1989
A;Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for multiple forms of the enzyme
A;Reference number: JN0588; MUID:90128276; PMID:2612911
A;Accession: JN0588
A;Molecule type: mRNA
A;Residues: 1-499 <TSU>
A;Cross-references: UNIPROT:Q96TH4
C;Comment: The alpha amylases are encoded by multigene family.
C;Genetics:

A;Gene: Taa-G1
A;Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <MAT>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 13; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13

Db 99 AYHGYWQDIYSL 111

RESULT 7

B48305
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: B48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.; Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspergillus awamori
A;Reference number: A48305; MUID:90254827; PMID:2340591

A;Accession: B48305
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-499 <KOR>
A;Cross-references: UNIPROT:Q02906
C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 13; DB 2; Length 499;

Best Local Similarity 100.0%; Pred. No. 3.2e-08; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13

Db 99 AYHGYWQDIYSL 111

RESULT 8

A35282
alpha-amylase (EC 3.2.1.1) - Aspergillus niger
C;Species: Aspergillus niger
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35282
R;Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pet. Biochemistry 29, 6244-6249, 1990
A;Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom
A;Reference number: A35282; MUID:91002514; PMID:2207069
A;Accession: A35282

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-484 <BOE>
C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;173-300/Domain: alpha-amylase core homology <AMY>

Query Match 61.5%; Score 8; DB 1; Length 484;

Best Local Similarity 100.0%; Pred. No. 0.03; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQ 8

Db 78 AYHGYWQ 85

RESULT 9

T41560
phenylalanyl-trna synthetase - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T41560
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21991
A:Accession: T41560
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-429 <WOO>
A:Cross-references: UNIPROT:O74952; EMBL:AL023705; PIDN:CAAL19267.1; GSPDB:GN000068; SPDB:
A:Experimental source: strain 972h-; cosmid c736
C:Genetics:
A:Gene: SPDB:SPCC736.03c
A:Map position: 3
C:Superfamily: phenylalanine-tRNA ligase alpha chain

Query Match 46.2%; Score 6; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QDIYSL 13
Db 203 QDIYSL 208

RESULT 10
T40860
probable alpha-amylase precursor SPCC11E10.09c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40860; T41181
R:Rampersger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21952
A:Accession: T40860
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-478 <RAM>
A:Cross-references: UNIPROT:Q10427; EMBL:AL121783; NID:G6016988; PIDN:CAB57851.1; PID:96
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, April 1999
A:Reference number: Z21976
A:Accession: T41181
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-203 <LYN>
A:Cross-references: EMBL:AL049662; NID:G4678680; PIDN:CAB41221.1; PID:G4678681; GSPDB:GN
A:Experimental source: strain 972h-; cosmid c188
C:Genetics:
A:Gene: SPDB:SPCC11E10.09c; SPDB:SPCC188.01c
A:Map position: 3
A:Introns: 320/3; 468/3
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 46.2%; Score 6; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 89 AYHGYW 94

RESULT 11
S31478
alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C:Species: Thermoactinomyces vulgaris
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S31478
R:Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; H
submitted to the EMBL Data Library, December 1992
A:Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A:Reference number: S31478

A:Accession: S31478
A:Molecule type: DNA
A:Residues: 1-482 <HOF>
A:Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:G48289; PIDN:CAA49465.1; PID:G4829
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:194-319/Domain: alpha-amylase core homology <AMY>

Query Match 46.2%; Score 6; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 107 AYHGYW 112

RESULT 12
G75392
glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: G75392
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75392
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-483 <WHI>
A:Cross-references: UNIPROT:O9RU88; GB:AE001991; GB:AE000513; NID:G6459223; PIDN:AAF110
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRI472
A:Map position: 1
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 46.2%; Score 6; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
Db 101 AYHGYW 106

RESULT 13
T38448
probable alpha-amylase precursor - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38448
R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21749
A:Accession: T38448
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-491 <MUR>
A:Cross-references: UNIPROT:O13936; EMBL:Z98978; PIDN:CAB11675.1; GSPDB:GN000066; SPDB:S
A:Experimental source: strain 972h-; cosmid c27E2
C:Genetics:
A:Gene: SPDB:SPAC27E2.01
A:Map position: 1
A:Introns: 325/3; 476/3
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 46.2%; Score 6; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
| | | | |
DB 94 AYHGYW 99

RESULT 14
ALBYAF
alpha-amylase (EC 3.2.1.1) precursor - yeast (Saccharomycopsis fibuligera)
C;Species: Saccharomycopsis fibuligera
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S00064
R;Itoh, T.; Yamashita, I.; Fukui, S.
FEBS Lett. 219, 339-342, 1987
A;Title: Nucleotide sequence of the alpha-amylase gene (ALP1) in the yeast Saccharomycop
A;Reference number: S00064; MUID:87276512; PMID:3457057
A;Accession: S00064
A;Molecule type: DNA
A;Residues: 1-494 <ITO>
A;Cross-references: UNIPROT:P21567; EMBL:X05791; NID:94847; PIDN:CAA29233.1; PID:94848
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 368-Thr
C;Genetics:
A;Gene: ALP1
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; extracellular protein; glycoprotein; glycosidase; hydrolase; metall
P;1-26/Domain: signal sequence #status predicted <SIG>
P;27-494/Product: alpha-amylase #status predicted <MAT>
F;200-327/Domain: alpha-amylase core homology <AMY>
F;57-65,177-191,262-493/Disulfide bonds: #status predicted
F;148,189,202,237/Binding site: calcium (Asn, Gln, Asp, His) #status predicted
P;224/Binding site: carbohydrate (Asn) (covalent) #status predicted
P;233,257,324/Active site: Asp, Glu, Asp #status predicted

Query Match 46.2%; Score 6; DB 1; Length 494;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
| | | | |
DB 105 AYHGYW 110

RESULT 15
S33921
alpha-amylase (EC 3.2.1.1) SWA2 precursor - yeast (Schwanniomyces occidentalis)
N;Alternate names: alpha-1,4 glucanohydrolase
C;Species: Schwanniomyces occidentalis
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S33921
R;Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genet. 24, 75-83, 1993
A;Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase fro
A;Reference number: S33921; MUID:93365041; PMID:8358835
A;Accession: S33921
A;Molecule type: DNA
A;Residues: 1-507 <CLA>
A;Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g3965
C;Genetics:
A;Gene: SWA2
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
P;1-20/Domain: signal sequence #status predicted <SIG>
P;21-507/Product: alpha-amylase #status predicted <MAT>
P;205-332/Domain: alpha-amylase core homology <AMY>

F;134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 46.2%; Score 6; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYW 6
| | | | |
DB 110 AYHGYW 115

Search completed: November 7, 2005, 19:33:47
Job time : 1.58108 secs

It's Egg Bunk (1994)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:00:20 ; Search time 6.90154 Seconds
(without alignment)
964.571 Million cell updates/sec

Title: US-10-820-200-2_COPY_98_110
Perfect score: 13
Sequence: 1 AHHGWMQDIYSL 13

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	100.0	498	1 AMYA ASPAW	Q02905 aspergillus
2	13	100.0	498	2 Q76CT3	Q76CT3 aspergillus
3	13	100.0	499	1 AMYA ASPOR	P10529 aspergillus
4	13	100.0	499	1 AMYA ASPAW	Q02906 aspergillus
5	13	100.0	499	1 AMYA ASPSH	P30292 aspergillus
6	13	100.0	499	2 Q96TH4	Q96TH4 aspergillus
7	13	100.0	499	2 Q76L99	Q76L99 aspergillus
8	13	100.0	499	2 Q7LV45	Q7LV45 aspergillus
9	11	84.6	490	2 Q9UV07	Q9UV07 emericella
10	10	76.9	128	2 O15751	O15751 dictyosteli
11	8	61.5	484	1 AMYA ASPNG	P56271 aspergillus
12	8	61.5	634	2 Q76L96	Q76L96 aspergillus
13	8	61.5	640	2 O13296	O13296 aspergillus
14	6	46.2	322	2 Q6Y198	Q6Y198 picchia angu
15	6	46.2	413	2 Q9MER9	Q9MER9 malus domes
16	6	46.2	415	2 Q6CDK9	Q6CDK9 yarrowia li
17	6	46.2	429	2 Q74952	Q74952 schizosacch
18	6	46.2	478	1 YQ29 SCHPO	O10427 schizosacch
19	6	46.2	482	2 Q60051	Q60051 thermoactin
20	6	46.2	483	2 Q9RUB8	Q9RUB8 deinococcus
21	6	46.2	491	2 O13396	O13396 schizosacch
22	6	46.2	494	1 AMY1 SACFI	Q8RIQ6 saccharomyc
23	6	46.2	503	2 Q8RIQ6	Q8RIQ6 fusbobacteri
24	6	46.2	507	1 AMY2 DEBOC	Q08806 debaryomyce
25	6	46.2	512	1 AMY1 DEBOC	P19269 debaryomyce
26	6	46.2	512	2 Q7P5Z5	Q7P5Z5 fusbobacteri
27	6	46.2	513	1 AMY3 SCHPO	O14154 schizosacch
28	6	46.2	514	1 TUP1 CANAL	P56093 candida alb
29	6	46.2	527	2 Q8VYH3	Q8VYH3 arabidopsis
30	6	46.2	528	1 AMY_BACCI	P08137 bacillus ci
31	6	46.2	552	2 Q9LVM8	Q9LVM8 arabidopsis

32	6	46.2	564	1 AMY4 SCHPO	Q9Y7S9 schizosacch
33	6	46.2	583	2 Q874K2	Q874K2 penicillium
34	6	46.2	604	1 RCO1 NEUCR	P78706 neurospora
35	6	46.2	604	2 Q7SBB8	Q7SBB8 neurospora
36	6	46.2	607	2 Q6BY06	Q6BY06 debaryomyce
37	6	46.2	614	1 TUI1 SCHPO	Q097L5 schizosacch
38	6	46.2	619	2 Q6J0W8	Q6J0W8 exophiala d
39	6	46.2	619	2 Q9HGL0	Q9HGL0 emericella
40	6	46.2	624	1 AMY1 LIPKO	Q01117 lipomyces k
41	6	46.2	625	2 Q74922	Q74922 schizosacch
42	6	46.2	629	2 Q751E0	Q751E0 ashbya goss
43	6	46.2	631	2 Q92394	Q92394 cryptococcu
44	6	46.2	643	2 Q6FWR0	Q6FWR0 candida gla
45	6	46.2	647	2 Q8WZL8	Q8WZL8 yarrowia li

ALIGNMENTS

RESULT 1
ID AMYA ASPAW STANDARD; PRT; 498 AA.
AC Q02905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DS glucanohydrolase A).
GN Name=AMVA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
from Aspergillus niger var. awamori.",
RL Curr. Genet. 17:203-212(1990).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -I- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X52755; CAA36966.1; -
CC FIR; A48305; A48305.
CC HSSP; P10529; 7TAA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
CC Hydroxylase; Multigene family; Signal.
CC SIGNAL 1 21 Potential.
CC CHAIN 22 498 Alpha-amylase A.
CC FT ACT SITE 227 227 Nucleophile (By similarity).
CC FT ACT SITE 251 251 Proton donor (By similarity).
CC FT ACT SITE 318 318 By similarity.
CC FT METAL 142 142 Calcium 1 (By similarity).

```

FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 498 AA; 54880 MW; 765851BC01A8A01 CRC64;
Query Match 100.0%; Score 13; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AYHGYYQQDIYSL 13
Db 99 AYHGYYQQDIYSL 111
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RESULT 2
Q76CT3 PRELIMINARY; PRT; 498 AA.
AC Q76CT3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase.
GN Names=amyA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito K.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB109452; BAD01051.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;
Query Match 100.0%; Score 13; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AYHGYYQQDIYSL 13
Db 98 AYHGYYQQDIYSL 110
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RESULT 3
AMYA ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
DE alpha-D-glucan glucanohydrolase).
GN Name=AMY1;
GN and
GN Name=AMY2;

```

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GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RC MEDLINE=89237897; PubMed=2785629;
RA Wiersel S., Lachmund A., Wildhardt G., Ruttkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RT Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kiritani N., Tsuboi A., Udaoka S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RC MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";
RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RC MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RC MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RC MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzozowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.

```

CC -1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations.
 CC -1- SUBUNIT: Monomer.
 CC -1- BIOTECHNOLOGY: Used in the brewing industry to increase the
 CC fermentability of beer worts (including those made from unmalted
 CC cereals), in the starch industry to make high maltose and high DE
 CC syrups (starch saccharification), in the alcohol industry to
 CC reduce fermentation time, in the cereal food industry for flour
 CC supplementation and improvement of chilled and frozen dough, and
 CC in the forestry industry for low-temperature modification of
 CC starch. Sold under the name Fungamyl by Novozymes.
 CC -1- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC -----
 CC EMBL; X12725; CAA31218.1; --
 CC EMBL; X12726; CAA31219.1; --
 CC EMBL; X12727; CAA31220.1; --
 CC EMBL; D00434; BAA00336.1; --
 CC EMBL; M33218; AAA32708.1; --
 CC PIR; JK0201; JK0201.
 CC PIR; JT0466; JT0466.
 CC PIR; S04548; ALAS1.
 CC PDB; 2TAA; X-ray; A=22-499.
 CC PDB; 6TAA; X-ray; Q=22-499.
 CC PDB; 7TAA; X-ray; Q=22-499.
 CC GlycoSuiteDB; F10529; --
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; Alpha-amy1ase; 1.
 CC PRINTS; PR00110; ALPHAAMYLASE.
 CC SMART; SM00642; Amy; 1.
 CC 3D-structure; Calcium-binding; Carbohydrate metabolism;
 CC Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 CC Multigene family; Signal.
 CC SIGNAL
 CC 1 21
 CC CHAIN 22 499 Alpha-amy1ase A.
 CC ACT_SITE 227 227 Nucleophile.
 CC ACT_SITE 251 251 Proton donor.
 CC ACT_SITE 318 318
 CC METAL 142 142 Calcium 1.
 CC METAL 183 183 Calcium 1 (via carbonyl oxygen).
 CC METAL 196 196 Calcium 1.
 CC METAL 227 227 Calcium 2.
 CC METAL 231 231 Calcium 1 (via carbonyl oxygen).
 CC METAL 251 251 Calcium 2.
 CC DISULFID 51 59
 CC DISULFID 171 185
 CC DISULFID 261 304
 CC DISULFID 461 496
 CC CARBOHYD 218 218 N-linked (GLCNAC...).
 CC FTID-CAR_000125.
 CC Q -> R (in AMY3).
 CC F -> L (in AMY3).
 CC TT -> DC (in Ref. 5).
 CC Q -> T (in Ref. 5).
 CC D -> Y (in Ref. 3).
 CC P -> L (in Ref. 3).
 CC G -> V (in Ref. 3).
 CC D -> H (in Ref. 4).
 CC I -> L (in Ref. 5).
 CC L -> A (in Ref. 4).
 CC WPIY -> PYI (in Ref. 5).
 CC G -> S (in Ref. 5).
 CC S -> SD (in Ref. 5 and 7).
 CC 497

FT HELIX 24 27
 FT TURN 28 29
 FT STRAND 32 35
 FT HELIX 37 40
 FT STRAND 42 42
 FT TURN 43 44
 FT HELIX 53 55
 FT STRAND 61 61
 FT HELIX 63 68
 FT TURN 69 69
 FT HELIX 70 74
 FT TURN 75 77
 FT STRAND 80 83
 FT STRAND 87 89
 FT STRAND 94 94
 FT TURN 95 96
 FT STRAND 97 97
 FT TURN 100 101
 FT STRAND 105 111
 FT TURN 113 114
 FT HELIX 118 130
 FT TURN 131 132
 FT STRAND 134 139
 FT STRAND 143 143
 FT STRAND 146 148
 FT HELIX 150 152
 FT HELIX 155 157
 FT STRAND 159 159
 FT STRAND 164 166
 FT HELIX 167 167
 FT STRAND 172 172
 FT TURN 176 177
 FT HELIX 179 184
 FT STRAND 186 188
 FT STRAND 192 194
 FT STRAND 195 197
 FT TURN 199 200
 FT HELIX 202 219
 FT TURN 220 220
 FT STRAND 223 226
 FT HELIX 229 231
 FT TURN 234 235
 FT HELIX 236 244
 FT TURN 245 245

Query Match 100.0%; Score 13; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQDIYSL 13
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 Db 99 AYHGYWQDIYSL 111

RESULT 4
 AMYB ASPAW STANDARD; PRT; 499 AA.
 ID AMYB ASPAW
 AC Q02906;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amy1ase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase B).
 GN Name=AMYB;
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=105351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UVK143F;
 RX MEDLINE=90254827; PubMed=2340591;
 RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,

RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
 RT "Cloning, characterization, and expression of two alpha-amylase genes
 RL from *Aspergillus niger* var. awamori.";
 RL Curr. Genet. 17:203-212(1990).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides
 CC -1- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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 CC -----
 DR EMBL; X52756; CAA36967.1; -;
 DR PIR; B48305; B48305.
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp amyl cat sub.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Multigene family; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 499 Alpha-amylase B.
 FT ACT_SITE 227 227 Nucleophile (By similarity).
 FT ACT_SITE 251 251 Proton donor (By similarity).
 FT ACT_SITE 318 318 By similarity.
 FT METAL 142 142 Calcium 1 (By similarity).
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 499 AA; 54921 MW; 740B96B11BC01A8A CRC64;
 Query Match 100.0%; Score 13; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVHGYWQDIYSL 13
 Db |||||
 99 AVHGYWQDIYSL 111
 RESULT 5
 AMY ASPSH STANDARD; PRT; 499 AA.
 ID ANY ASPSH
 AC P30292;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase)..
 GN Name=AMY;
 OS Aspergillus shirousami.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5070;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92323146; PubMed=1368777;
 RA Shibuya I., Tamura G., Ishikawa T., Hara S.;
 RT "Cloning of the alpha-amylase cDNA of *Aspergillus shirousami* and its
 RL expression in *Saccharomyces cerevisiae*.";
 RL Biosci. Biotechnol. Biochem. 56:174-179(1992).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
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 CC -----
 DR EMBL; D10461; BAA01255.1; -;
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp amyl cat sub.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Signal.
 FT SIGNAL 1 21 Alpha-amylase.
 FT CHAIN 22 499 Nucleophile (By similarity).
 FT ACT_SITE 227 227 Proton donor (By similarity).
 FT ACT_SITE 251 251 By similarity.
 FT ACT_SITE 318 318 Calcium 1 (By similarity).
 FT METAL 142 142 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 183 183 Calcium 1 (By similarity).
 FT METAL 196 196 Calcium 1 (By similarity).
 FT METAL 227 227 Calcium 2 (By similarity).
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 251 251 Calcium 2 (By similarity).
 FT DISULFID 51 59 By similarity.
 FT DISULFID 171 185 By similarity.
 FT DISULFID 261 304 By similarity.
 FT DISULFID 461 496 By similarity.
 FT CARBOHYD 218 218 N-linked (GlcNAc...) (By similarity).
 SQ SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;
 Query Match 100.0%; Score 13; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 8.3e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AVHGYWQDIYSL 13
 Db |||||
 99 AVHGYWQDIYSL 111
 RESULT 6
 Q96TH4 PRELIMINARY; PRT; 499 AA.
 ID Q96TH4
 AC Q96TH4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Taka-amylase A (EC 3.2.1.1).
 GN Name=amyA;
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RIE40;
RX MEDLINE=20289310; PubMed=10830498;
RA Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
gene, amyR, involved in the amylolytic gene expression in *Aspergillus
oryzae*."
RL Biosci. Biotechnol. Biochem. 64:816-827(2000).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB021876; BAA95703.1; -.
DR PIR; JN0588; JN0588.
DR PIR; S04549; ALAS3.
DR HSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; BEE42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 13; DB 2; Length 499;

Best Local Similarity 100.0%; Pred. No. 8.3e-07;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13

|||||

Db 99 AYHGYWQDIYSL 111

RESULT 7

Q76L99 PRELIMINARY; PRT; 499 AA.
AC Q76L99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
GN Name-amyl 1;
OS *Aspergillus awamori*.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
OX NCBI_TaxID=105351;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB083159; BA06002.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;

Query Match 100.0%; Score 13; DB 2; Length 499;

Best Local Similarity 100.0%; Pred. No. 8.3e-07;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13

|||||

Db 99 AYHGYWQDIYSL 111

RESULT 8

Q7LV45 PRELIMINARY; PRT; 499 AA.
AC Q7LV45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN Name-amyl;
OS *Aspergillus flavus*.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
OX NCBI_TaxID=5059;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-10D;
RA Fakhoury A.M., Woloshuk C.P.;
RT "Amyl, the alpha-amylase gene of *Aspergillus flavus*: Involvement in
RT aflatoxin biosynthesis in maize kernels.";
RL Phytopathology 89:908-914(1999).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF139255; AAF14264.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; BEE42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 13; DB 2; Length 499;

Best Local Similarity 100.0%; Pred. No. 8.3e-07;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYHGYWQDIYSL 13

|||||

Db 99 AYHGYWQDIYSL 111

RESULT 9

Q9UV07 PRELIMINARY; PRT; 490 AA.
AC Q9UV07;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-amylase AmyA.
GN Name-amylA;
OS *Emmericella nidulans* (*Aspergillus nidulans*).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; *Emmericella*.
OX NCBI_TaxID=162425;
[1]
RP SEQUENCE FROM N.A.
RA Boase N.A., Murphy R.M., Kelly J.M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF208225; AAF17103.1; -.
DR HSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.

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DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 490 AA; 54249 MW; A891C4ACEABE5305 CRC64;

Query Match      84.6%; Score 11; DB 2; Length 490;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AHGYWQDIY 11
   |||||
DB 91 AHGYWQDIY 101

RESULT 10
O15751 PRELIMINARY; PRT; 128 AA.
AC O15751;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AmyA (Fragment).
GN Name=amyA;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycotozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Loomis W.F., Iranfar N.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020284; AAB70852.1; -.
DR HSSP; P10529; TAA.
DR DictyBase; DDB0214924; amyA.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; Alpha-amyase; 1.
FT NON_TER 1
FT NON_TER 128
FT NON_TER 128
SQ SEQUENCE 128 AA; 14950 MW; 2ACE8FDC5E79637 CRC64;

Query Match      76.9%; Score 10; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YHGYWQDIY 11
   |||||
DB 3 YHGYWQDIY 12

RESULT 11
AMYA ASPNG STANDARD; PRT; 484 AA.
AC P56271;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acid alpha-amyase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=91002514; PubMed=2207069;
RA Boel E., Brady L., Brzozowski A.M., Derewenda Z., Dodson G.G.,
RA Jensen V.J., Petersen S.B., Swift H., Thim L., Woldike H.F.;
RT "Calcium binding in alpha-amyases: an X-ray diffraction study at 2.1-
RT A resolution of two enzymes from Aspergillus."
RL Biochemistry 29:6244-6249(1990).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.

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CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
DR PDB; 2AAA; X-ray; @=1-484.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; Alpha-amyase; 1.
DR SMART; SM00642; Amy; 1.
KW 3D-structure; Calcium-binding; Carbohydrate metabolism; Glycoprotein;
KW Glycosidase; Hydrolase.
FT ACT_SITE 206 206 Nucleophile.
FT ACT_SITE 230 230 Proton donor.
FT ACT_SITE 297 297
FT METAL 121 121 Calcium 1.
FT METAL 162 162 Calcium 1 (via carbonyl oxygen).
FT METAL 175 175 Calcium 1.
FT METAL 206 206 Calcium 2.
FT METAL 210 210 Calcium 1 (via carbonyl oxygen).
FT METAL 230 230 Calcium 2.
FT DISULFID 30 38
FT DISULFID 150 164
FT DISULFID 240 283
FT DISULFID 440 475
FT CARBOHYD 24 24
FT CARBOHYD 157 157
FT CARBOHYD 197 197
FT HELIX 3 6
FT TURN 7 8
FT STRAND 11 13
FT HELIX 16 19
FT TURN 22 23
FT HELIX 32 34
FT HELIX 42 47
FT TURN 48 48
FT HELIX 49 53
FT TURN 54 56
FT TURN 59 62
FT STRAND 66 68
FT STRAND 73 73
FT TURN 74 75
FT STRAND 76 76
FT TURN 79 80
FT STRAND 84 90
FT TURN 92 94
FT HELIX 97 108
FT TURN 109 111
FT STRAND 113 118
FT STRAND 122 122
FT STRAND 125 125
FT HELIX 129 131
FT HELIX 134 136
FT STRAND 138 138
FT HELIX 143 145
FT STRAND 146 146
FT STRAND 151 151
FT TURN 155 156
FT HELIX 158 163
FT STRAND 165 167
FT STRAND 172 173
FT STRAND 175 176
FT TURN 178 179
FT HELIX 181 198
FT TURN 199 199
FT STRAND 202 205
FT TURN 209 210
FT HELIX 213 215
FT HELIX 216 223
FT TURN 224 224
FT STRAND 226 229
FT HELIX 236 239
FT TURN 240 244
FT TURN 245 245
FT STRAND 248 250
FT HELIX 252 262

```

FT TURN 265 266
FT HELIX 269 282
FT HELIX 286 288
FT STRAND 290 291
FT TURN 296 297
FT HELIX 301 303
FT TURN 304 304
FT HELIX 308 320
FT STRAND 324 328
FT TURN 329 334
FT TURN 339 343
FT HELIX 347 350
FT TURN 351 352
FT TURN 354 355
FT HELIX 357 375
FT TURN 377 381
FT STRAND 385 390
FT TURN 391 392
FT STRAND 393 398
FT TURN 401 403
FT STRAND 405 410
FT TURN 414 415
FT STRAND 419 423
FT TURN 430 431
FT STRAND 433 436
FT TURN 437 440
FT STRAND 441 444
FT TURN 447 448
FT STRAND 451 455
FT TURN 457 458
FT STRAND 461 465
FT HELIX 466 469
FT TURN 470 471
FT TURN 474 475
SQ SEQUENCE 484 AA; 52935 MW; 04D596E34680656D CRC64;

Query Match 61.5%; Score 8; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.38; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQQ 8
|||||||
DB 78 AYHGYWQQ 85

RESULT 12
ID Q76L96 PRELIMINARY; PRT; 634 AA.
AC Q76L96;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylose precursor.
GN Name=amyl III;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083162; BAD06005.1; -.
DR EMBL; AB083160; BAD06003.1; -.
DR HSSP; P04064; IACZ.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylose; 1.
DR Q76L96;
DR PROD; PD001568; Glyco_Hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 640 AA; 69507 MW; 676BF9D0236720DD CRC64;

Query Match 61.5%; Score 8; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQQ 8
|||||||
DB 99 AYHGYWQQ 106

RESULT 14
ID Q6Y198 PRELIMINARY; PRT; 322 AA.
AC Q6Y198;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TUP1-like protein (Fragment).
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.

DR Pfam; PF00686; CBM_20; 1.
DR PROD; PD001568; Glyco_Hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 634 AA; 69242 MW; 16C0BE6AF6FB0E9B CRC64;
Query Match 61.5%; Score 8; DB 2; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQQ 8
|||||||
DB 99 AYHGYWQQ 106

RESULT 13
ID O13296 PRELIMINARY; PRT; 640 AA.
AC O13296;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acid-stable alpha-amylose.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko A., Sudo S., Sakamoto Y., Tamura G., Ishikawa T., Ohba T.;
RT "Molecular-cloning and determination of the nucleotide-sequence of a
RT gene encoding an acid-stable alpha-amylose from Aspergillus-
RT kawachii.";
RL J. Ferment. Bioeng. 81:292-298(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Kaneko A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008370; BAA22993.1; -.
DR HSSP; P56271; 2AAA.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR002044; Glyco_hydro_CBD.
DR Pfam; PF00128; Alpha-amylose; 1.
DR PROD; PD001568; Glyco_Hydro_CBD; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 640 AA; 69507 MW; 676BF9D0236720DD CRC64;

Query Match 61.5%; Score 8; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 0.46; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYHGYWQQ 8
|||||||
DB 99 AYHGYWQQ 106

RESULT 14
ID Q6Y198 PRELIMINARY; PRT; 322 AA.
AC Q6Y198;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TUP1-like protein (Fragment).
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.

Search completed: November 7, 2005, 19:32:39
Job time : 7.90154 secs

OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE FROM N.A.
RA Oliveira M.A., Salmazo A.P.T., Faria V.G., Pereira G.A.G.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 7 WD repeats.
DR EMBL; AV145087; AAN60571.1; -.
DR InterPro; IPR001690; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 6.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS00082; WD_REPEATS_2; 6.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON TER 1
FT NON TER 322 322
SQ SEQUENCE 322 AA; 35083 MW; 017CADD0E0E9B03 CRC64;

Query Match 46.2%; Score 6; DB 2; Length 322;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QDIYSL 13
Db 99 QDIYSL 104

RESULT 15
Q9M6R9 PRELIMINARY; PRT; 413 AA.
AC Q9M6R9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fruit;
RX MEDLINE=20156234; PubMed=10691968;
RA Wegryn T., Reilly K., Cipriani G., Murphy P., Newcomb R., Gardner R.,
RA MacRae E.;
RT "A novel alpha-amylase gene is transiently upregulated during low
RT temperature exposure in apple fruit."
RL Eur. J. Biochem. 287:1313-1322(2000).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF153828; AAF63239.1; -.
DR HSSP; P04063; 1BG9.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 413 AA; 46883 MW; C77763D797B6D0EA CRC64;

Query Match 46.2%; Score 6; DB 2; Length 413;
Best Local Similarity 100.0%; Pred.No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 QDIYSL 13
Db 77 QDIYSL 82

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:24:00 ; Search time 3.75676 Seconds
(without alignments)
954.162 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 40

Sequence: 1 SSQDYFH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	ID	Description
1	40	100.0	498	1 AMYA ASPAW	Q02905 aspergillus
2	40	100.0	498	2 Q76CT3	Q76ct3 aspergillus
3	40	100.0	499	1 AMYA ASPOR	P10529 aspergillus
4	40	100.0	499	1 AMYA ASPAW	Q02906 aspergillus
5	40	100.0	499	1 AMY ASPSH	P30292 aspergillus
6	40	100.0	499	2 Q96TH4	Q96th4 aspergillus
7	40	100.0	499	2 Q76L99	Q76l99 aspergillus
8	40	100.0	499	2 Q7LV45	Q7lv45 aspergillus
9	40	100.0	624	1 AMY1_LIPKO	Q01117 lipomyces k
10	40	100.0	647	2 Q6YF33	Q6yf33 lipomyces s
11	37	92.5	224	2 Q70BE3	Q70be3 pseudomonas
12	36	90.0	596	2 Q78L16	Q78l16 plasmodium
13	36	90.0	627	2 Q6ENF7	Q6fnf7 candida gla
14	35	87.5	760	2 Q7R038	Q7r038 giardia lam
15	35	87.5	760	2 Q9XZJ0	Q9xzf0 giardia lam
16	34	85.0	130	2 Q23373	Q23373 arabidopsis
17	34	85.0	7048	2 Q6D739	Q6d739 erwinia car
18	33	82.5	125	2 Q751X1	Q751x1 ashbya gos
19	33	82.5	193	2 Q8LMS1	Q8lms1 oryza sativ
20	33	82.5	248	2 Q7YSZ6	Q7yvez6 rhodnius pr
21	33	82.5	257	2 Q6P396	Q6p396 mus musculu
22	33	82.5	370	2 Q8BYC0	Q8byc0 mus musculu
23	33	82.5	420	2 Q39309	Q39309 equid herpe
24	33	82.5	420	2 Q55525	Q55525 equid herpe
25	33	82.5	585	1 C9C9_MOUSE	Q9d718 mus musculu
26	33	82.5	601	2 O17552	O17552 caenorhabdi
27	33	82.5	762	2 Q7NAH6	Q7nah6 mycoplasma
28	33	82.5	1131	1 DNEB1_HHV7J	P52339 human herpe
29	33	82.5	1131	2 Q56282	Q56282 human herpe
30	33	82.5	1304	2 Q6FR07	Q6fr07 candida gla
31	33	82.5	1731	2 Q9P230	Q9p230 homo sapien

32	33	82.5	3124	2	Q96L91	Q96l91 homo sapien
33	33	82.5	4351	1	FAT2_RAT	Q88277 rattus norv
34	32	80.0	49	2	Q6XYZ7	Q6xyz7 spiroplasma
35	32	80.0	95	2	Q7RM89	Q7rm89 plasmodium
36	32	80.0	144	1	AGH_ARMVU	Q9u8r2 armadillidi
37	32	80.0	163	2	Q9CUQ8	Q9cuq8 mus musculu
38	32	80.0	180	2	Q97SK2	Q97sk2 streptococc
39	32	80.0	181	2	Q7USU1	Q7usu1 rhodopirell
40	32	80.0	183	2	Q8DZ39	Q8dz39 streptococc
41	32	80.0	183	2	Q8E4P7	Q8e4p7 streptococc
42	32	80.0	215	2	P97975	P97975 unidentifie
43	32	80.0	218	2	Q9CUH8	Q9cuh8 mus musculu
44	32	80.0	255	2	Q8EU15	Q8eu15 oceanobacil
45	32	80.0	261	2	Q73L56	Q73l56 treponema d

ALIGNMENTS

RESULT 1

ID	AMYA ASPAW	STANDARD;	PRT;	498 AA.
AC	Q02905;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Alpha-amylase A precursor (SC 3.2.1.1) (1,4-alpha-D-glucan			
DE	glucanohydrolase A).			
GN	Name=AMVA;			
OS	Aspergillus awamori.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
OX	NCBI_TaxID=105351;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=UVK143F;			
RX	MEDLINE=90254827; PubMed=2340591;			
RA	Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,			
RA	Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;			
RT	"Cloning, characterization, and expression of two alpha-amylase genes			
RT	from Aspergillus niger var. awamori.";			
RL	Curr. Genet. 17:203-212(1990).			
CC	- - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic			
CC	linkages in oligosaccharides and polysaccharides.			
CC	- - COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory			
CC	at high concentrations (By similarity).			
CC	- - SIMILARITY: Belongs to the glycosyl hydrolase 13 family.			
CC				
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CC	or send an email to license@isb-sib.ch).			
CC				
CC	EMBL; X52755; CAA36966.1; -.			
DR	PIR; A48305; A48305.			
DR	HSP; P10529; 7TAA.			
DR	InterPro; IPR006589; Alp_ amyl_cat_sub.			
DR	InterPro; IPR006047; Alpha_amyl_cat.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; Alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAAMYLASE.			
DR	SMART; SM00642; Amyv; 1.			
KW	Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;			
KW	Hydrolase; Multigene family; Signal.			
FT	SIGNAL 1 21			
FT	CHAIN 22 498			
FT	ACT_SITE 227 227			
FT	ACT_SITE 251 251			
FT	ACT_SITE 318 318			
FT	ACT_SITE 142 142			
FT	METAL			

```

FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT METAL 196 196 similarity).
FT METAL 227 227 Calcium 1 (By similarity).
FT METAL 231 231 Calcium 2 (By similarity).
FT METAL 251 251 Calcium 1 (via carbonyl oxygen) (By
FT METAL 251 251 similarity).
FT DISULFID 51 59 Calcium 2 (By similarity).
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 498 AA; 54880 MW; 7658511BC01A9A01 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 2
O76CT3 PRELIMINARY; PRT; 498 AA.
AC O76CT3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase.
GN Name=amyA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP Ito K.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
RL -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC EMBL; AB109452; BAD1051.1; -.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 3
AMYA ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
DE alpha-D-glucan glucanohydrolase).
GN Name=AMY1;
GN and
GN Name=AMY2;

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GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RC MEDLINE=89237897; PubMed=2785629;
RA Wirsel S., Lachmund A., Wildhardt G., Rutkowski E.;
RA "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RA "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RL Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Uda S.;
RA "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RL A with trypsin and chymotrypsin.";
RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RC MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RC MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RC MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzozowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.

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CC -|- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations.
 CC -|- SUBUNIT: Monomer.
 CC -|- BIOTECHNOLOGY: Used in the brewing industry to increase the
 CC fermentability of beer worts (including those made from unmalted
 CC cereals), in the starch industry to make high maltose and high DE
 CC syrups (starch saccharification), in the alcohol industry to
 CC reduce fermentation time, in the cereal food industry for flour
 CC supplementation and improvement of chilled and frozen dough, and
 CC in the forestry industry for low-temperature modification of
 CC starch. Sold under the name Fungamyl by Novozymes.
 CC -|- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
 CC -|- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC -----
 CC EMBL; X12725; CAA31218.1; -;
 CC EMBL; X12726; CAA31219.1; -;
 CC EMBL; X12727; CAA31220.1; -;
 CC EMBL; D00434; BAA00336.1; -;
 CC EMBL; M33218; AAA32708.1; -;
 CC PIR; JK0201; JK0201.
 CC PIR; JT0466; JT0466.
 CC PIR; S04548; ALAS1.
 CC PDB; 2TAA; X-ray; A=22-499.
 CC PDB; 6TAA; X-ray; @=22-499.
 CC PDB; 7TAA; X-ray; @=22-499.
 CC GlycoSuiteDB; P10529; -;
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC Pfam; PF00128; Alpha-amy1ase; 1.
 CC PRINTS; PR00110; ALPHAAMYLAASE.
 CC SMART; SM00642; Aamy; 1.
 CC 3D-structure; Calcium-binding; Carbohydrate metabolism;
 KW Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
 KW Multigene family; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 499 Alpha-amy1ase A.
 FT ACT_SITE 227 227 Nucleophile.
 FT ACT_SITE 251 251 Proton donor.
 FT ACT_SITE 318 318
 FT METAL 142 142 Calcium 1.
 FT METAL 183 183 Calcium 1 (via carbonyl oxygen).
 FT METAL 196 196 Calcium 1.
 FT METAL 227 227 Calcium 2.
 FT METAL 231 231 Calcium 1 (via carbonyl oxygen).
 FT METAL 251 251 Calcium 2.
 FT DISULFID 51 59
 FT DISULFID 171 185
 FT DISULFID 261 304
 FT DISULFID 461 496
 FT CARBOHYD 218 218 N-linked (GlcNAc...).
 FT VARIANT 56 56 /FTID=CAR_000125.
 FT VARIANT 172 172 Q -> R (in AMY3).
 FT CONFLICT 93 94 F -> L (in AMY3).
 FT CONFLICT 106 106 TT -> DC (in Ref. 5).
 FT CONFLICT 184 184 Q -> Y (in Ref. 5).
 FT CONFLICT 195 195 D -> T (in Ref. 3).
 FT CONFLICT 255 255 P -> L (in Ref. 3).
 FT CONFLICT 291 291 D -> V (in Ref. 3).
 FT CONFLICT 345 345 D -> H (in Ref. 4).
 FT CONFLICT 370 370 I -> L (in Ref. 5).
 FT CONFLICT 406 409 L -> A (in Ref. 4).
 FT CONFLICT 448 448 WPIY -> PYI (in Ref. 5).
 FT CONFLICT 497 497 G -> S (in Ref. 5).
 FT S -> SD (in Ref. 5 and 7).

FT HELIX 24 27
 FT TURN 28 29
 FT STRAND 32 35
 FT HELIX 37 40
 FT STRAND 42 42
 FT TURN 43 44
 FT HELIX 53 55
 FT STRAND 61 61
 FT HELIX 63 68
 FT TURN 69 69
 FT HELIX 70 74
 FT TURN 75 77
 FT STRAND 80 83
 FT STRAND 87 89
 FT STRAND 94 94
 FT TURN 95 96
 FT STRAND 97 97
 FT TURN 100 101
 FT STRAND 105 111
 FT TURN 113 114
 FT HELIX 118 130
 FT TURN 131 132
 FT STRAND 134 139
 FT STRAND 143 143
 FT STRAND 146 148
 FT HELIX 150 152
 FT HELIX 155 157
 FT STRAND 159 159
 FT STRAND 164 166
 FT HELIX 167 167
 FT STRAND 172 172
 FT TURN 176 177
 FT HELIX 179 184
 FT STRAND 186 188
 FT STRAND 192 194
 FT STRAND 196 197
 FT TURN 199 200
 FT TURN 202 219
 FT TURN 220 220
 FT STRAND 223 226
 FT HELIX 229 231
 FT TURN 234 235
 FT HELIX 236 244
 FT TURN 245 245

Query Match 100.0%; Score 40; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 162 SSQDYFH 168

RESULT 4
 AMYB ASPAW STANDARD; PRT; 499 AA.
 ID AMYB ASPAW
 AC Q02906;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amy1ase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase B).
 GN Name=AMYB;
 OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=105351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UVK143F;
 RX MEDLINE=90254827; PubMed=2340591;
 RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,

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SEQUENCE FROM N.A.
RP RX MEDLINE=92323146; PubMed=1368777;
RA Shibuya I., Tamura G., Ishikawa T., Hara S.;
RT "Cloning of the alpha-amylase cDNA of Aspergillus shiroyamii and its
RT expression in Saccharomyces cerevisiae.";
RL Biosci. Biotechnol. Biochem. 56:174-179(1992).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
-----
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-----
CC EMBL: D10461; BAA01255.1; -.
CC DR HSPG; P10529; 7TAA.
CC DR InterPro: IPR006599; Alp_amyl_cat_sub.
CC DR InterPro: IPR006047; Alpha_amyl_cat.
CC DR InterPro: IPR006046; Glyco_hydro_13.
CC PFAM: PF00128; Alpha-amylase; 1.
CC DR PRINTS; PR00110; ALPHAAMYLASE.
CC DR SMART; SM00642; Amy; 1.
CC KX Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Signal.
FT SIGNAL 1 21
FT CHAIN 22 499
FT ACT_SITE 227 227
FT ACT_SITE 251 251
FT ACT_SITE 318 318
FT ACT_SITE 318 318
FT METAL 142 142
FT METAL 183 183
FT METAL 196 196
FT METAL 227 227
FT METAL 231 231
FT METAL 251 251
FT DISULFID 51 59
FT DISULFID 171 185
FT DISULFID 261 304
FT DISULFID 461 496
FT CARBOHYD 218 218
FT SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;
Query Match 100.0%; Score 40; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
DB 162 SSQDYFH 168
-----
RESULT 6
Q96TH4 PRELIMINARY; PRT; 499 AA.
ID Q96TH4 AC Q96TH4;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Taka-amylase A (EC 3.2.1.1).
GN Name=amvA;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]

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Db 162 SSQDYFH 168

RESULT 8

Q7LV45 PRELIMINARY; PRT; 499 AA.

AC Q7LV45

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Alpha-amylase (EC 3.2.1.1).

GN Name:amyl;

OS Aspergillus flavus.

OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Eurotiomycetes;

OC Eukariotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI_TaxID=5059;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=86-10D;

RA Fakhoury A.M., Woloshuk C.P.;

RT "Amy1, the alpha-amylase gene of Aspergillus flavus: Involvement in

RL aflatoxin biosynthesis in maize kernels.";

CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

DR EMBL; AF139925; AAF14264.1; -.

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_amyl_cat.

DR InterPro; IPR006589; Alp_amyl_cat_sub.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; Alpha-amylase; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

DR SMART; SM00642; Amy; 1.

KW Glycosidase; Hydrolase.

SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 499;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 SSQDYFH 7

Db 162 SSQDYFH 168

RESULT 9

AMY1_LIPKO STANDARD; PRT; 624 AA.

ID AMY1_LIPKO

AC Q01117;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan

DE Glucanohydrolase 1).

GN Name=LXAI;

OS Lipomyces kononenkoae.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Lipomycetaceae; Lipomyces.

OX NCBI_TaxID=34357;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IGC4052B;

RX MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;

RA Steyn A.J.C., Marmur J., Pretorius I.S.;

RT "Cloning, sequence analysis and expression in yeasts of a cDNA

RL containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";

RL Gene 166:65-71(1995).

RN [2]

RP SEQUENCE OF 29-44.

RC STRAIN=IGC4052B;

RX MEDLINE=96132108; PubMed=8593683;

RA Steyn A.J.C., Pretorius I.S.;

RT "Characterization of a novel alpha-amylase from *Lipomyces kononenkoae*
 RT and expression of its gene (LKAL) in *Saccharomyces cerevisiae*.";
 RL Curr. Genet. 28:526-533(1995).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides
 CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -!- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
 CC domain.
 CC -----
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 CC -----
 CC EMBL; U30376; AAC49622.1; ALT_INIT.
 CC PIR; JC4510; JC4510.
 CC DR HSSP; P10529; 7TAA.
 CC DR InterPro; IPR006589; Alp_amyl_cat_sub.
 CC DR InterPro; IPR006047; Alpha_amyl_cat.
 CC DR InterPro; IPR005036; CBM 21.
 CC DR Pfam; PF00128; Alpha-amylase; 1.
 CC DR Pfam; PF03370; CBM 21; 1.
 CC DR SMART; SM00642; Amy; 1.
 CC KX Calcium-binding; Carbohydrate metabolism; Direct protein sequencing;
 KW Glycoprotein; Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 624 Alpha-amylase 1.
 FT DOMAIN 40 133 Carbohydrate binding type-21.
 FT ACT_SITE 353 Nucleophile (By similarity).
 FT ACT_SITE 377 Proton donor (By similarity).
 FT ACT_SITE 444 By similarity.
 FT METAL 268 Calcium 1 (By similarity).
 FT METAL 309 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 322 Calcium 1 (By similarity).
 FT METAL 353 Calcium 2 (By similarity).
 FT METAL 357 Calcium 1 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 377 Calcium 2 (By similarity).
 FT DISULFID 177 185 By similarity.
 FT DISULFID 297 311 By similarity.
 FT DISULFID 387 430 By similarity.
 FT DISULFID 587 622 By similarity.
 FT CARBOHYD 304 304 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 344 344 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 624 AA; 68876 MW; 87EB16534F5A9A9F CRC64;

Query Match 100.0%; Score 40; DB 1; Length 624;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 Db 288 SSQDYFH 294
 |||||

RESULT 10
 Q6YF33 PRELIMINARY; PRT; 647 AA.
 AC Q6YF33;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Alpha-amylase.
 OS *Lipomyces starkeyi*.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Lipomycetaceae; Lipomyces.

OX NCBI_TaxID=29829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KSM 22M;
 RX PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
 RA Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
 RA Moon T.-W.;
 RT "Cloning and expression of *Lipomyces starkeyi* alpha-amylase in
 RT *Escherichia coli* and determination of some of its properties.";
 RT FEMS Microbiol. Lett. 233:53-64(2004).
 DR EMBL; AY155463; AAN75021.1; --
 DR HSSP; P26827; 1A47.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR005036; CBM 21.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR Pfam; PF03370; CBM 21; 1.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 647;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 Db 311 SSQDYFH 317
 |||||

RESULT 11
 Q70BE3 PRELIMINARY; PRT; 224 AA.
 ID Q70BE3
 AC Q70BE3;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Putative helicase.
 OS *Pseudomonas syringae* (pv. tomatol).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fanelli V., Finetti-Sialer M., Gallitelli D.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AJ604589; CAES4310.1; --
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00271; Helicase_C; 1.
 KW Helicase.
 SQ SEQUENCE 224 AA; 25431 MW; 8701280423194015 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 224;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 Db 130 STQDYFH 136
 |||||

RESULT 12
 Q7RL16 PRELIMINARY; PRT; 596 AA.
 ID Q7RL16
 AC Q7RL16;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE *Drosophila melanogaster* CG11926 gene product, putative

(Fragment).
 DE Name=PY02732;
 OS Plasmodium yoelii yoelii.
 OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17XNL;
 RX PubMed=1236865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anguolli S.V., Suh B.B., Kooij T.W., Perteu M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519 (2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AABL01000756; EAA22214.1; -.
 DR InterPro; IPR004353; Yeast73DUF.
 DR Pfam; PF03164; DUF254; 1.
 DR PRINTS; PR01546; YEAST73DUF.
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 Best Local Similarity 85.7%; Pred. No. 87;
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 QY 1 SSQDYFH 7
 Db 446 SSQDFFH 452
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 AC Q6FNF7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Candida glabrata strain CBS138 chromosome K complete sequence.
 GN ORFNames=CAGL0K002979;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=284593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anchoard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaud J.M., Nikolaki M., Ostas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";

RL Nature 430:35-44 (2004).
 DR EMBL; CR380957; CAG61198.1; -.
 DR InterPro; IPR002013; SyJa_N.
 DR Pfam; PF02383; SyJa_N; 1.
 DR PROSITE; PS0275; SAC; 1.
 SQ SEQUENCE 627 AA; 71471 MW; DEAOB02466F4F480 CRC64;
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 Best Local Similarity 85.7%; Pred. No. 92;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 7
 Db 365 SSQDYFH 371
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 AC Q7R038;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GLP 456 15756 18038.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
 OC NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACB01000038; EAA40649.1; -.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF0023; ANK; 3.
 DR PRINTS; PR01415; ANKYRIN.
 SQ SEQUENCE 760 AA; 85474 MW; A01440ACE754099C CRC64;
 Query Match 87.5%; Score 35; DB 2; Length 760;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 Db 5 SSQDWFH 11
 RESULT 15
 ID Q9XZJ0 PRELIMINARY; PRT; 760 AA.
 AC Q9XZJ0;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ankyrin-like protein.
 OS Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
 OX NCBI_TaxID=5741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Portland;
 RA Sekyere E.O., Edwards M.R., Stewart T.S., Schofield P.J., Knodler L.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF144322; AAD28486.1; -.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ANK; 3.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 3.

KW ANK repeat.
SQ SEQUENCE 760 AA; 85542 MW; 12B54841019CD475 CRC64;
Query Match 87.5%; Score 35; DB 2; Length 760;
Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 5 SSQDWFH 11

Search completed: November 7, 2005, 18:52:32
Job time : 5.75676 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 17:47:24 ; Search time 1.05405 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 40

Sequence: 1 SSQDYFH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	478	1	US-08-720-899-7
2	40	100.0	478	1	US-08-459-610-7
3	40	100.0	478	2	US-08-343-804-7
4	40	100.0	478	2	US-08-339-715A-2
5	40	100.0	478	2	US-08-600-908A-10
6	40	100.0	478	3	US-08-683-838A-10
7	40	100.0	478	3	US-09-182-859-7
8	40	100.0	478	4	US-09-672-459-7
9	40	100.0	478	4	US-09-636-252A-10
10	40	100.0	478	4	US-10-186-042-7
11	33	82.5	180	4	US-09-248-796A-22820
12	32	80.0	84	4	US-09-583-110-4016
13	32	80.0	95	4	US-09-107-433-4442
14	32	80.0	369	1	US-08-700-359-21
15	32	80.0	583	2	US-08-616-392C-4
16	32	80.0	788	4	US-09-107-532A-6538
17	32	80.0	792	4	US-09-134-000C-5895
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19	32	80.0	1118	4	US-09-949-016-6596
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21	31	77.5	153	4	US-09-328-352-4170
22	31	77.5	279	4	US-09-270-767-34772
23	31	77.5	279	4	US-09-270-767-49989
24	31	77.5	461	4	US-09-198-452A-924
25	31	77.5	472	4	US-09-438-185A-858
26	31	77.5	474	4	US-09-081-385-148
27	31	77.5	2697	4	US-10-144-198-12

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30	30	75.0	25	2	US-08-484-211C-41	Sequence 41, Appl
31	30	75.0	25	3	US-08-906-769-41	Sequence 41, Appl
32	30	75.0	25	3	US-08-906-616-41	Sequence 41, Appl
33	30	75.0	25	3	US-08-817-795-41	Sequence 41, Appl
34	30	75.0	25	3	US-08-485-443B-41	Sequence 41, Appl
35	30	75.0	25	3	US-08-639-075A-41	Sequence 41, Appl
36	30	75.0	25	3	US-09-012-431-41	Sequence 41, Appl
37	30	75.0	25	3	US-09-012-692-41	Sequence 41, Appl
38	30	75.0	25	3	US-08-906-613-41	Sequence 41, Appl
39	30	75.0	25	5	PCT-US95-1442A-41	Sequence 41, Appl
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44	30	75.0	64	3	US-08-906-616-75	Sequence 75, Appl
45	30	75.0	64	3	US-08-817-795-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 23-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-720-899-7

Query Match 100.0%; Score 40; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 2
US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,610
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match 100.0%; Score 40; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/339,715A-2
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-343-804-7

Query Match 100.0%; Score 40; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 4
US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriki, Takashi
; APPLICANT: Yanase, Michio
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993
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; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Melser, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-715A-2

Query Match 100.0%; Score 40; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 5
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; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169 No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-683-838A-10

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Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 7
US-09-182-859-7
; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisg rd-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
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; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7

Query Match 100.0%; Score 40; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
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Db 141 SSQDYFH 147

RESULT 8
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match 100.0%; Score 40; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
|||
Db 141 SSQDYFH 147

RESULT 9
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A

; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10

Query Match 100.0%; Score 40; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
|||
Db 141 SSQDYFH 147

RESULT 10
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 100.0%; Score 40; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
|||
Db 141 SSQDYFH 147

RESULT 11
US-09-248-796A-22820
; Sequence 22820, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 22820
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-22820

Query Match 82.5%; Score 33; DB 4; Length 180;
 Best Local Similarity 83.3%; Pred. No. 40;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYFH 7
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 DB 102 NQDYFH 107

RESULT 12
 US-09-583-110-4016
 ; Sequence 4016, Application US/09583110
 ; Patent No. 6699703
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 ; FILE REFERENCE: PATH00-07A
 ; CURRENT APPLICATION NUMBER: US/09/583,110
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/107,433
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/085,131
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: US 60/051,553
 ; PRIOR FILING DATE: 1997-07-02
 ; NUMBER OF SEQ ID NOS: 5322
 ; SEQ ID NO 4016
 ; LENGTH: 84
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-583-110-4016

Query Match 80.0%; Score 32; DB 4; Length 84;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
 :|||||
 DB 40 QDYFH 44

RESULT 13
 US-09-107-433-4442
 ; Sequence 4442, Application US/09107433
 ; Patent No. 6800744
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 ; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
 ; THERAPEUTICS
 ; NUMBER OF SEQUENCES: 5206
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02354
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-ROM ISO9660
 ; COMPUTER: <Unknown>
 ; OPERATING SYSTEM: <Unknown>

; SOFTWARE: <Unknown>
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107,433
 ; FILING DATE: 30-Jun-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/ 085131
 ; FILING DATE: May 12, 1998
 ; APPLICATION NUMBER: 60/051553
 ; FILING DATE: July 2, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ariniello, Pamela Deneke
 ; REGISTRATION NUMBER: 40,489
 ; REFERENCE/DOCKET NUMBER: GTC-011
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781)893-5007
 ; TELEFAX: (781)893-8277
 ; INFORMATION FOR SEQ ID NO: 4442:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 95 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: Streptococcus pneumoniae
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (B) LOCATION 1...95
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4442:
 US-09-107-433-4442

Query Match 80.0%; Score 32; DB 4; Length 95;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
 :|||||
 DB 51 QDYFH 55

RESULT 14
 US-08-700-359-21
 ; Sequence 21, Application US/08700359
 ; Patent No. 5766925
 ; GENERAL INFORMATION:
 ; APPLICANT: SUGIMOTO, MASAKAZU
 ; APPLICANT: USUDA, YOSHIHIRO
 ; APPLICANT: SUZUKI, TOMOKO
 ; APPLICANT: TANAKA, AKIHO
 ; APPLICANT: MATSUI, HIROSHI
 ; TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MS-DOS TEXT EDITOR
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,359
 ; FILING DATE: 08-OCT-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP-35019
 ; FILING DATE: 04-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: NORMAN F. OBLON

/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 10-819-0 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-413-3000
/ TELEFAX: 703-413-2220
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 369 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-700-359-21

Query Match 80.0%; Score 32; DB 1; Length 369;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 133 SSMDYFH 139

RESULT 15
US-08-616-392C-4
/ Sequence 4, Application US/08616392C
/ Patent No. 5998165
/ GENERAL INFORMATION:
/ APPLICANT: Goold, Richard D.
/ APPLICANT: Akerblom, Ingrid E.
/ APPLICANT: Seilhamer, Jeffrey
/ APPLICANT: Coleman, Roger
/ TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES PANC1A
/ TITLE OF INVENTION: AND PANC1B ASSOCIATED WITH PANCREATIC CANCER
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/616,392C
/ FILING DATE: 15-MAR-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/581,240
/ FILING DATE: 29-DEC-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0052-1US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 583 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: hnt
/ CLONE: 496071
/ US-08-616-392C-4

Query Match 80.0%; Score 32; DB 2; Length 583;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 433 STDDYFH 439

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Job time : 2.05405 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:11:05 ; Search time 3.7973 Seconds
(without alignments)
771.303 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 40

Sequence: 1 SSQDYFH 7

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Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	40	100.0	478	14	US-10-184-771-10
3	40	100.0	478	14	US-10-186-042-7
4	40	100.0	478	15	US-10-644-187-7
5	40	100.0	478	17	US-10-926-720-10
6	40	100.0	478	17	US-10-980-759-7
7	40	100.0	478	20	US-11-064-196-10
8	40	100.0	498	16	US-10-815-495-22
9	40	100.0	498	16	US-10-820-200-2
10	40	100.0	498	17	US-10-877-849-30
11	40	100.0	499	16	US-10-815-495-18

12	40	100.0	499	16	US-10-797-393A-5	Sequence 5, Appli
13	40	100.0	608	17	US-10-877-849-40	Sequence 40, Appl
14	40	100.0	640	17	US-10-877-849-36	Sequence 36, Appl
15	40	100.0	1095	14	US-10-228-063-45	Sequence 45, Appl
16	34	85.0	256	14	US-10-298-638-16	Sequence 16, Appl
17	33	82.5	133	15	US-10-424-599-175172	Sequence 175172,
18	33	82.5	133	15	US-10-424-599-218859	Sequence 218859,
19	33	82.5	167	16	US-10-767-701-39199	Sequence 39199, A
20	33	82.5	193	16	US-10-437-963-140941	Sequence 140941,
21	33	82.5	697	16	US-10-425-115-275630	Sequence 275630,
22	33	82.5	703	15	US-10-425-114-65668	Sequence 65668, A
23	33	82.5	1731	17	US-10-732-923-8855	Sequence 8855, Ap
24	33	82.5	3124	17	US-10-732-923-8854	Sequence 8854, Ap
25	33	82.5	4351	10	US-09-970-944-20	Sequence 20, Appl
26	32	80.0	71	15	US-10-424-599-162174	Sequence 162174,
27	32	80.0	79	16	US-10-425-115-187129	Sequence 187129,
28	32	80.0	86	16	US-10-425-115-355307	Sequence 355307,
29	32	80.0	95	18	US-10-617-320-4442	Sequence 4442, Ap
30	32	80.0	119	15	US-10-264-049-4124	Sequence 4124, Ap
31	32	80.0	152	16	US-10-425-115-271310	Sequence 271310,
32	32	80.0	180	17	US-10-472-928-496	Sequence 496, App
33	32	80.0	323	15	US-10-282-122A-72639	Sequence 72639, A
34	32	80.0	501	18	US-10-450-763-45485	Sequence 45485, A
35	32	80.0	529	20	US-11-097-143-39465	Sequence 39465, A
36	32	80.0	583	9	US-09-924-654-4	Sequence 4, Appli
37	32	80.0	594	9	US-09-925-300-1079	Sequence 1079, Ap
38	32	80.0	820	15	US-10-369-493-686	Sequence 686, App
39	32	80.0	820	15	US-10-282-122A-42805	Sequence 42805, A
40	32	80.0	820	15	US-10-282-122A-74838	Sequence 74838, A
41	32	80.0	820	15	US-10-282-122A-75391	Sequence 75391, A
42	32	80.0	820	15	US-10-272-107-3	Sequence 3, Appli
43	32	80.0	820	17	US-10-689-395-3	Sequence 3, Appli
44	32	80.0	885	16	US-10-437-963-136212	Sequence 136212,
45	32	80.0	1118	14	US-10-153-668-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-10-877-849-43
; Sequence 43, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877, 849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

Query Match 100.0%; Score 40; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

Db 141 SSQDYFH 147

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RESULT 2
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1f216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 1996-07-18
; PRIOR APPLICATION NUMBER: 08/683,838
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10
Query Match 100.0%; Score 40; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 3
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7
Query Match 100.0%; Score 40; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 4
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7
Query Match 100.0%; Score 40; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 5
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
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; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 100.0%; Score 40; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 6

US-10-980-759-7
; Sequence 7, Application US/10980759
; Publication No. US20050118695A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/980,759
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-980-759-7

Query Match 100.0%; Score 40; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 7

US-11-064-196-10
; Sequence 10, Application US/11064196
; Publication No. US20050170487A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants

; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/11/064,196
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-11-064-196-10

Query Match 100.0%; Score 40; DB 20; Length 478;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 8

US-10-815-495-22
; Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 100.0%; Score 40; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 9

US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Pedersen, Sven
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2

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; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match      100.0%; Score 40; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
    |||||
Db 161 SSQDYFH 167

RESULT 10
US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match      100.0%; Score 40; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
    |||||
Db 161 SSQDYFH 167

RESULT 11
US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connelly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match      100.0%; Score 40; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
    |||||
```

```
Db 162 SSQDYFH 168

RESULT 12
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Pestersen, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match      100.0%; Score 40; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
    |||||
Db 162 SSQDYFH 168

RESULT 13
US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

Query Match      100.0%; Score 40; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
    |||||
Db 161 SSQDYFH 167

RESULT 14
US-10-877-849-36
; Sequence 36, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
```

; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 40; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
|||
Db 161 SSQDYFH 167

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lananan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 100.0%; Score 40; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
|||
Db 141 SSQDYFH 147

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Job time : 4.7973 secs

The Page Book (1900)

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:55 ; Search time 4.02703 Seconds
(without alignments)
672.288 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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1: Geneseqp19808:*
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3: Geneseqp20008:*
4: Geneseqp20018:*
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6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	423	4	ABB09072 Aspergill
2	7	100.0	478	2	AAR46065 Mutant al
3	7	100.0	478	2	AAR72450 Aspergill
4	7	100.0	478	2	AAR78270 Aspergill
5	7	100.0	478	2	AAR79025 Mature ta
6	7	100.0	478	2	AAW14500 Aspergill
7	7	100.0	498	4	AAB84206 Amino aci
8	7	100.0	498	8	ADT99632 Aspergill
9	7	100.0	499	8	ADT99628 Aspergill
10	7	100.0	1095	6	ABP96630 Alpha-amy
11	6	85.7	182	5	ABP28341 Streptoco
12	6	85.7	351	8	ADG61605 Transcrip
13	6	85.7	493	2	AAR88212 Alpha-amy
14	5	71.4	45	4	AAW24481 Human EST
15	5	71.4	52	4	AAO08447 Human pol
16	5	71.4	61	4	AAO02433 Human pol
17	5	71.4	69	4	ABJ15756 Human ner
18	5	71.4	84	8	ADK47501 Streptoco
19	5	71.4	88	4	ABB08450 Human pho
20	5	71.4	94	4	ABB71558 Drosophil
21	5	71.4	95	4	AAG64127 Human TNF
22	5	71.4	95	8	ADR95807 Novel S.
23	5	71.4	104	3	AAV90470 Yeast Sml
24	5	71.4	119	4	AAU31764 Novel hum
25	5	71.4	123	4	AAO08298 Human pol

26	5	71.4	128	5	ABB98330	Subtilisi
27	5	71.4	131	4	AAO03876	Human pol
28	5	71.4	134	7	ADD19267	Human sec
29	5	71.4	151	7	ADK52505	Penicilli
30	5	71.4	154	2	AAV30848	Human sec
31	5	71.4	180	6	ABU00681	S. pneumo
32	5	71.4	180	8	ADM92084	S. pneumo
33	5	71.4	185	5	ABP26186	Streptoco
34	5	71.4	189	6	ABP76858	N. gonorr
35	5	71.4	189	6	ABP78080	N. gonorr
36	5	71.4	222	4	AAU31887	Novel hum
37	5	71.4	222	8	ADQ66002	Novel hum
38	5	71.4	255	3	AAG33176	Zea may
39	5	71.4	280	3	AAG33175	Zea may
40	5	71.4	286	3	AAG33174	Zea may
41	5	71.4	298	6	ABU16660	Protein e
42	5	71.4	303	6	ADA33877	Aginetoba
43	5	71.4	317	7	ADC95026	E. faeciu
44	5	71.4	326	6	ABP98616	Mature Br
45	5	71.4	330	4	AAB96495	Putative

ALIGNMENTS

RESULT 1
ABB09072
ID ABB09072 standard; protein; 423 AA.
XX
AC ABB09072;
XX
DT 26-JUN-2002 (first entry)
XX
DE Aspergillus oryzae TAKA protein (TAA).
XX
KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
KW protein co-ordinate data; 3 dimensional structure.
XX
OS Aspergillus oryzae.
XX
PN KR2001027418-A.
XX
PD 06-APR-2001.
XX
PF 09-SEP-1999; 99KR-00039130.
XX
PR 09-SEP-1999; 99KR-00039130.
XX
PA (POST-) POSTECH FOUND.
PA (SAMY-) SAMYANG GENEX CORP.
PI Kim TJ, Park GH;
DR WPI; 2001-534477/59.
XX
PT Manufacturing maltogenic amylase having improved transglycosylation
PT activity, comprises using crystallization.
XX
PS Disclosure; Page 188; 196pp; Korean.
XX
CC The present invention describes manufacturing maltogenic amylase (EC
CC 3.2.1.133) having improved transglycosylation activity, comprising using
CC crystallisation and the three dimensional structure of maltogenic
CC amylase. Manufacturing maltogenic amylase comprises the following steps:
CC (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC
CC 5027BP) and inserting the gene into plasmid pUC19 to construct
CC recombinant DNA (pHMA119); (ii) inserting the recombinant DNA to
CC Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius
CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
CC supernatant through column chromatography and obtaining purified
CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two

CC maltogenic amylase molecules, and a *Thermus* sp. IM6501 maltogenic amylase
 CC (ThMA) crystal. The amylase has a structure containing an activated
 CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
 CC and a pocket with glucose bound that consists of amino acid residues of
 CC Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn131, Glu132, Val1329,
 CC and His1360. The present sequence represents *Aspergillus oryzae* TAKA
 CC protein (TAA), given in comparison with ThMA in the present invention
 XX
 SQ Sequence 423 AA;

Query Match 100.0%; Score 7; DB 4; Length 423;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 137 SSQDYFH 143

RESULT 2
 AAR46065
 ID AAR46065 standard; protein; 478 AA.
 XX
 AC AAR46065;

XX
 XX
 DT 25-MAR-2003 (revised)
 DT 18-JUL-1994 (first entry)
 XX

DE Mutant alpha-amylase.

XX Methionine substitution; stability; activity; detergent;
 KW dishwashing agents; liquefaction agents.
 XX
 OS *Aspergillus oryzae*.

XX
 PN WO9402597-A1.
 XX
 PD 03-FEB-1994.

XX
 PF 06-JUL-1993; 93WO-DK000230.
 XX
 PR 23-JUL-1992; 92DK-00000946.
 PR 16-DEC-1992; 92DK-00001503.
 PR 15-MAR-1993; 93DK-00000292.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A, Bisgard-Frantzen H;
 XX
 DR WPI; 1994-048855/06.

XX Mutant alpha-amylase from *Bacillus* species comprising a methionine
 PT substitution - with improved stability and activity at low pH, for use in
 PT detergents, dishwashing agents and liquefaction agents.
 XX

PS Claim 1; Page 7; 20pp; English.

XX The sequence os that of the *Aspergillus oryzae* alpha amylase, sold
 CC commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be
 CC mutated by substitution of one or more of its methionine residues for any
 CC amino acid other than cysteine. The mutant alpha-amylase exhibits a
 CC better activity level and better stability in the presence of oxidising
 CC agents than previous mutant alpha amylases, and improved thermostability
 CC at moderately low pH. The enzyme can be used as an additive for
 CC detergents, dishwashing agents and liquefaction agents. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 478 AA;

Query Match 100.0%; Score 7; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 141 SSQDYFH 147
 RESULT 3
 AAR72450
 ID AAR72450 standard; protein; 478 AA.
 XX
 AC AAR72450;

XX
 XX
 DT 25-MAR-2003 (revised)
 DT 01-DEC-1995 (first entry)
 XX

DE *Aspergillus oryzae* alpha amylase (mature protein).

XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
 KW washing; *Bacillus licheniformis*; *Bacillus amyloliquefaciens*;
 KW *Bacillus stearothermophilus*; dyeing; bleaching; scouring; textile;
 KW thermostable.

XX *Aspergillus oryzae*.

XX WO9510603-A1.

XX PD 20-APR-1995.

XX PF 05-OCT-1994; 94WO-DK000370.

XX PR 08-OCT-1993; 93DK-00001133.

XX PR 02-FEB-1994; 94DK-00000140.

XX (NOVO) NOVO-NORDISK AS.

XX Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
 PI Van Der Zee P;
 XX
 XX WPI; 1995-161790/21.

XX New *Bacillus* derived alpha-amylase variants - having amino acid
 PT modifications to improve washing and/or dishwashing performance.

PS Disclosure; Page 75-76; 105pp; English.

XX Variant alpha amylase enzymes which have improved washing and/or as
 CC detergent additives. The enzymes have one or more amino acid residues
 CC added, deleted or substituted. The variants can also be used for textile
 CC desizing prior to scouring, bleaching and dyeing. The variants have
 CC improved thermostability, acid/alkaline stability; low temperature
 CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
 CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
 CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 478 AA;

Query Match 100.0%; Score 7; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 141 SSQDYFH 147

RESULT 4
 AAR78270
 ID AAR78270 standard; protein; 478 AA.
 XX
 AC AAR78270;

XX
 XX
 DT 17-JAN-1996 (first entry)
 XX
 DE *Aspergillus oryzae* alpha amylase (mature protein).

```

XX Alpha amylase; oxidation; desizing; bleaching; scouring; fabric; starch;
KW thermocable; methionine; Bacillus licheniformis;
KW Bacillus amyloliquefaciens; Bacillus stearothermophilus;
KW Aspergillus oryzae.
XX
OS Aspergillus oryzae.
XX
PN WO9521247-A1.
XX
PD 10-AUG-1995.
XX
PF 05-OCT-1994; 94WO-DK000371.
XX
PR 02-FEB-1994; 94DK-00000141.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Toft AH, Marcher D, Pedersen HH, Nilsson TE;
XX
DR WPI; 1995-283767/37.
XX
XX Use of an oxidation stable alpha-amylase - for simultaneous desizing and
PT bleaching or scouring of fabrics contg. starch or starch derivs.
XX
XX Disclosure; Page 25-26; 37pp; English.
XX
CC Oxidation stable alpha amylases can be used for the simultaneous desizing
CC and bleaching or scouring of a fabric comprising starch or starch
CC derivatives. They exhibit a better heat stability, especially in the
CC presence of oxidising agents. They are obtained from a parent alpha
CC amylase by replacing one or more methionine residues with any amino acid
CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
CC Asp. The parent alpha amylase is pref. derived from a Bacillus species,
CC although alpha amylases of fungal origin can also be used. This sequence
CC is the wild type (unmodified) alpha amylase of Aspergillus oryzae
XX
SQ Sequence 478 AA;

Query Match 100.0%; Score 7; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 5
AAR79025
ID AAR79025 standard; protein; 478 AA.
XX
AC AAR79025;
XX
XX
DT 22-MAR-1996 (first entry)
XX
DE Mature taka-amylase A.
XX
KW Wild type; neopullulanase; B. stearothermophilus; mutant; food industry;
KW modification; hydrophobicity; replacement insertion; deletion.
XX
OS Aspergillus oryzae.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 30..38
FT Disulfide-bond 150..164
FT Disulfide-bond 240..283
FT Disulfide-bond 439..474
XX
PN JP07177891-A.
XX
XX 18-JUL-1995.
XX

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```

PF 31-OCT-1994; 94JP-00288658.
XX
PR 12-NOV-1993; 93JP-00306096.
XX
XX (NIDE ) NEC CORP.
PA (EZAK ) EZAKI GLICO CO.
XX
XX WPI; 1995-279919/37.
XX
XX Modifying a transferase by enhancing hydrophobicity of a selected site -
PT increases transfer activity, also new mutant neo-pullulanase(s).
XX
XX Disclosure; Page 10-11; 18pp; English.
XX
CC This sequence represents the mature form of taka-amylase from A. oryzae.
CC This sequence was used in a method for the generation of mutant
CC pullulanases for use in the food industry (see also AAR79026-28). The
CC wild type pullulanase enzyme was modified by the method of the invention
CC for enhancing the hydrophobicity of a selected site of the pullulanase.
CC The method comprises replacement of a group in the selected site with a
CC hydrophobic group, replacement of an amino acid with a hydrophobic amino
CC acid, and/or insertion or deletion of a hydrophobic amino acid from the
CC selected site. The method was used to produce neopullulanases Y377F,
CC S422V and M375L
XX
XX Sequence 478 AA;

Query Match 100.0%; Score 7; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 6
AAW14500
ID AAW14500 standard; protein; 478 AA.
XX
AC AAW14500;
XX
XX
DT 04-JUN-1997 (first entry)
XX
DE Aspergillus oryzae alpha-amylase (mature protein).
XX
KW alpha-amylase; mature; Bacillus licheniformis; termamyl; fungamyl;
KW Aspergillus oryzae; Bacillus amyloliquefaciens; altered property;
KW calcium dependency; substrate binding; stability; pH optimum;
KW thermostability; cleavage; oligosaccharide substrate; dishwashing;
KW washing; detergent additive; fabric desizing; starch liquefaction;
KW sweetener; ethanol production; variant.
XX
OS Aspergillus oryzae.
XX
XX Key Location/Qualifiers
FH Misc-difference 13..45
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 7-23 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 33"
FT Misc-difference 14..40
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 8-18 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 35"
FT Misc-difference 28..42
FT /label= loop 1 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding

```

FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT
FT Misc-difference 32. .38
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 14-15 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 32"
FT
FT Misc-difference 66. .84
FT /label= loop 2 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 44-57 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 18"
FT
FT Misc-difference 70. .78
FT /label= loop 2 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 48-51 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 20"
FT
FT Misc-difference 98. .210
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 117-185 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 24"
FT
FT Misc-difference 102. .206
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 121-181 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 26"
FT
FT Misc-difference 121. .181
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to this fragment is deleted or replaced with a fragment
FT corresponding to 102-206 of AAW14499; claim 41"
FT
FT Misc-difference 121. .174
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to this fragment is deleted or
FT replaced with a fragment corresponding to 102-199 of
FT AAW14499; claim 42"
FT
FT Misc-difference 165. .177
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 195-202 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 21"
FT
FT Misc-difference 166. .173
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 196-198 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 23"
FT
FT Misc-difference 181. .184
FT /note= "an amino acid fragment corresponding to this
FT region is deleted from the parent sequence of a variant
FT Fungamyl; claim 43"
FT
FT Misc-difference 291. .313
FT /label= loop 8 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 322-346 of AAW14498 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 36"
FT
FT Misc-difference 297. .313
FT /label= loop 8 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for

FT a variant) corresponding to 325-345 of AAW14498 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 38"
FT
FT XX WO9623874-A1.
FT
FT XX 08-AUG-1996.
FT
FT XX 05-FEB-1996; 96WO-DK000057.
FT
FT XX 03-FEB-1995; 95DK-00000128.
FT
FT XX 23-OCT-1995; 95DK-00001192.
FT
FT XX 10-NOV-1995; 95DK-00001256.
FT
FT XX (NOVO) NOVO-NORDISK AS.
FT
FT XX Svendsen A, Bisgard-Frantzen H, Borchert TV;
FT WPI; 1996-371424/37.
FT
FT XX Alpha-amylase variants and methods of production - have altered
FT properties such as calcium dependency, substrate binding and stability.
FT
FT XX Disclosure; Page 87-88; 171pp; English.
FT
FT XX The present sequence is the mature Aspergillus oryzae alpha-amylase (A).
FT Variants of parent termamyl- and fungamyl-like alpha-amylases (and
FT methods of constructing them) are claimed. Examples of variants are
FT featured above. The variants have altered properties such as: calcium
FT dependency, substrate binding and stability. Also one or more proline or
FT cysteine residues in the variant is modified or replaced with a non-
FT proline or non-cysteine residue such as alanine. The variants can be used
FT for (dish)washing, as detergent additives or for fabric desizing or
FT starch liquerfaction. They can also be used for the production of
FT sweeteners and ethanol from starch. See also AAW14498-99
FT
FT XX Sequence 478 AA;
FT
FT Query Match 100.0%; Score 7; DB 2; Length 478;
FT Best Local Similarity 100.0%; Pred. No. 2.1;
FT Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT QY 1 SSQDYFH 7
FT |||||
FT 141 SSQDYFH 147
FT
FT Db
FT
FT RESULT 7
FT AAB84206
FT ID AAB84206 standard; protein; 498 AA.
FT
FT XX AAB84206;
FT
FT XX 06-AUG-2001 (first entry)
FT
FT XX Amino acid sequence of a fungamyl-like alpha-amylase.
FT
FT XX Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
FT alcohol; starch; dough improver; brewing; starch liquification.
FT
FT XX Aspergillus oryzae.
FT
FT XX WO200134784-A1.
FT
FT XX 17-MAY-2001.
FT
FT XX 10-NOV-2000; 2000WO-DK000626.
FT
FT XX 10-NOV-1999; 99DK-00001617.
FT
FT XX (NOVO) NOVOZYMES AS.
FT
FT XX Bisgard-Frantzen H, Svendsen A, Pedersen S;

XX WPI; 2001-367478/38.
DR N-PSDB; AAF90208.
XX
PT New variant of Fungamyl-like alpha-amylase, useful for production of
PT maltose syrups, includes mutations that improve stability against heat
PT and acidic pH.
XX
PS Claim 1; Page 42-45; 49pp; English.
XX
XX The present sequence represents a fungamyl-like alpha-amylase. The
CC specification describes variants of this fungamyl-like alpha-amylase,
CC which have an alteration in one the amino acid regions 98-110, 150-160,
CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
CC substitution of an amino acid or an insertion of an amino acid downstream
CC of a particular position. The variants retain alpha-amylase activity, and
CC have better heat stability and/or stability at acidic pH, relative to
CC wild-type enzyme. The variants can therefore be used at higher
CC temperatures (more efficient conversion or faster reaction, and have
CC reduced need for cooling and reduced risk of contamination). The variants
CC may also be used in conjunction with other enzymes, particularly
CC glucoamylase during dextrinisation. The variants are used to produce
CC syrups, particularly of high maltose content, or alcohol, from starch; as
CC dough improver for baked goods; in brewing, to increase fermentability of
CC the wort; and for liquefaction of starch
XX
SQ Sequence 498 AA;
Query Match 100.0%; Score 7; DB 4; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 161 SSQDYFH 167
|||||||
RESULT 8
ADT89632
ID ADT89632 standard; protein; 498 AA.
XX
AC ADT89632;
XX
DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
KW Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.
XX
OS Aspergillus niger.
XX
PN US2004191864-A1.
XX
PD 30-SEP-2004.
XX
PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX
DR WPI: 2004-708545/69.
XX
DR N-PSDB; ADT89631.
XX
PT Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX
XX Example 11; SEQ ID NO 22; 59pp; English.

CC The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequences encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX
SQ Sequence 498 AA;
Query Match 100.0%; Score 7; DB 8; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168
|||||||
RESULT 9
ADT89628
ID ADT89628 standard; protein; 499 AA.
XX
AC ADT89628;
XX
DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase B (amyB) protein.
XX
KW Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
XX
OS Aspergillus niger.
XX
PN US2004191864-A1.
XX
PD 30-SEP-2004.
XX
PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX
DR WPI: 2004-708545/69.
XX
DR N-PSDB; ADT89627.
XX
PT Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX
XX Example 10; SEQ ID NO 18; 58pp; English.
XX
XX The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous
CC biological substance, where mutant strain comprises first nucleotide
CC sequences encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase B (amyB) protein.
XX
SQ Sequence 499 AA;
Query Match 100.0%; Score 7; DB 8; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
|||||||

Db 162 SSQDYFH 168

RESULT 10
ABP96630
ID ABP96630 standard; protein; 1095 AA.
XX
AC ABP96630;
XX
DT 02-JUN-2003 (first entry)
XX
DE Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
XX
KW Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
KW pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW maltodextrin; ethanol; fermentation; beverage; enzyme.
XX
OS Aspergillus shiroyamii.
XX Synthetic.
XX
PN WO2003018766-A2.
XX
XX
PD 06-MAR-2003.
XX
PF 27-AUG-2002; 2002WO-US027129.
XX
XX 27-AUG-2001; 2001US-0315281P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Lanahan MB, Basu SS, Batie CJ, Chen W, Craig J, Kinkema M;
PI
DR WPI: 2003-268420/26.
DR N-PSDB; ACC44572.
XX
PT Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
PT alpha-amylase, useful for producing plant to produce food products having
PT improved taste or fermentable substrates for ethanol.
XX
PS Claim 1; Page 107; 158pp; English.
XX
CC The present invention describes polynucleotides which encode processing
CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
CC isomerase, or glucoamylase) that are optimised for expression in plants.
CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
CC processing enzymes, which are activated under suitable conditions to act
CC upon the desired substrate. Also described are self-processing transgenic
CC plants and plant parts, e.g. grain, which express one or more of these
CC enzymes and have an altered composition that facilitates plant and grain
CC processing. Also described is a method (M) for converting starch to
CC starch-derived products in a transformed plant part (TPP), by activating
CC the starch processing enzyme contained in it. Transgenic grain is useful
CC for preparing maltodextrin. A transformed plant (TP) can be used to
CC produce food products having improved taste and to produce fermentable
CC substrates for ethanol and fermented beverages. (M) eliminates the need
CC to mill or physically disrupt the integrity of plant parts prior to
CC recovery of starch-derived products. The present sequence represents
CC alpha-amylase/glucoamylase fusion protein, which is given in the
CC exemplification of the present invention
XX
SQ Sequence 1095 AA;
Query Match 100.0%; Score 7; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 4.2; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
RESULT 11

ABP28341
ID ABP28341 standard; protein; 182 AA.
XX
AC ABP28341;
XX
DT 02-JUL-2002 (first entry)
XX
DE Streptococcus polypeptide SEQ ID NO 5858.
XX
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS Streptococcus agalactiae.
XX
PN WO200234771-A2.
XX
PD 02-MAY-2002.
XX
PF 29-OCT-2001; 2001WO-GB004789.
XX
PR 27-OCT-2000; 2000GB-00026333.
PR 24-NOV-2000; 2000GB-00028727.
PR 07-MAR-2001; 2001GB-00005640.
XX
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
XX Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;
PI Tettelin H;
PI
DR WPI: 2002-352536/38.
DR N-PSDB; ABN68972.
XX
PT New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX
PS Claim 1; Page 3748; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC antibodies that bind (I) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (I) are used to detect Streptococcus in a
CC biological sample. (I) is used to determine whether a compound binds to
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (I) may be used to recombinantly produce (I) and may be
CC used in gene therapy. Antibodies to (I) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 182 AA;
Query Match 85.7%; Score 6; DB 5; Length 182;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYF 6
Db 134 SSQDYF 139
RESULT 12
AD061605
ID AD061605 standard; protein; 351 AA.
XX

AC ADO61605;
XX
DT 15-JUL-2004 (first entry)
DE Transcription factor G319, SEQ ID 72.
XX
KW Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KW osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
KW glyphosate resistance; flowering; fertility; seed development.
XX
OS Arabidopsis thaliana.
XX
PN WO2004031349-A2.
XX
PD 15-APR-2004.
XX
PF 18-SEP-2003; 2003WO-US030292.
XX
PR 18-SEP-2002; 2002US-0411837P.
PR 17-DEC-2002; 2002US-0434166P.
PR 24-APR-2003; 2003US-0465809P.
XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
XX Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
PI Riechmann JL, Haake V, Dubell AN, Keddle JS, Sherman BK;
XX
DR WPI; 2004-330163/30.
DR N-PSDB; ADO61604.
XX
XX New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PT properties compared to a reference plant.
XX
PS Claim 16; SEQ ID NO 72; 510pp; English.
XX
XX The present invention relates to novel plant transcription factor
CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
CC sequences can be used to produce transgenic plants, which overexpress
CC (II), where the transgenic plant has an altered trait as compared to a
CC non-transgenic plant or wild-type plant. The transgenic plant comprises
CC an altered trait selected from increased tolerance to abiotic stress,
CC increased tolerance to osmotic stress, increased tolerance to cold,
CC increased germination in cold, increased tolerance to heat, increased
CC germination in heat, increased tolerance to freezing conditions,
CC increased tolerance to low nitrogen conditions, increased tolerance to
CC low phosphate conditions, increased tolerance to disease, including
CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,
CC increased tolerance to multiple fungal pathogens, increased resistance to
CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
CC increased sensitivity to ACC, altered sugar sensing, increased tolerance
CC to sugars, altered carbon/nitrogen sensing, early flowering, late
CC flowering, altered flower structure, loss of flower determinacy, reduced
CC fertility, altered shoot meristem development, altered branching pattern,
CC altered stem morphology, altered vascular tissue structure, reduced
CC apical dominance, altered trichome density, altered trichome development,
CC altered trichome structure, altered root development, altered shade
CC avoidance, altered seed development, altered seed ripening, altered seed
CC germination, slow growth, fast growth, altered cell differentiation,
CC altered cell proliferation, altered cell expansion, altered phase change,
CC altered senescence, abnormal embryo development, altered programmed cell
CC death, lethality when overexpressed, altered necrosis patterns, increased
CC plant size, increased biomass, large seedlings, dwarfed plants, dark
CC green leaves, change in leaf shape, increased leaf size and mass, light
CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
CC altered seed coloration, altered seed size, altered seed shape, large
CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil
CC content, altered seed protein content, altered seedprenyl content,
CC altered leaf prenyl lipid content, increased anthocyanin levels, and
CC decreased anthocyanin levels. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 351 AA;
XX
Query Match 85.7%; Score 6; DB 8; Length 351;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYF 6
DB 226 SSQDYF 231
XX
RESULT 13
AAR88212
ID AAR88212 standard; protein; 493 AA.
XX
AC AAR88212;
XX
DT 16-OCT-2003 (revised)
DT 03-APR-1996 (first entry)
XX
DE Alpha-amylase.
XX
KW Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
XX
OS Thermomyces lanuginosus; CBS 224.63.
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT /label= Sig_peptide
XX
PN WO9601323-A1.
XX
XX 18-JAN-1996.
XX
XX 03-JUL-1995; 95WO-EP002607.
XX
PR 04-JUL-1994; 94GB-00013419.
XX
PA (DANI-) DANISCO AS.
XX
PI Michelsen B, Rasmussen P;
XX
XX WPI; 1996-087673/09.
DR N-PSDB; AAT10562.
XX
XX Thermophilic alpha-amylase with activity range of 60-80 degrees C.
PT derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
PT and bakery prods. esp. bread.
XX
PS Claim 3; Page 36-38; 94pp; English.
XX
XX A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS
CC 224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562)
CC isolated from a T. lanuginosus gene library. The recombinant enzyme (54-
CC 60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7
CC and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 493 AA;
XX
Query Match 85.7%; Score 6; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQDYFH 7
DB 162 SQDYFH 167
XX
RESULT 14
AAW24481

ID AAM24481 standard; protein; 45 AA.
XX AC AAM24481;
XX DT 12-OCT-2001 (first entry)
XX DE Human EST encoded protein SEQ ID NO: 2006.
XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US002687.
XX PR 25-JAN-2000; 2000US-00491404.
XX PR 17-JUL-2000; 2000US-00617746.
XX PR 03-AUG-2000; 2000US-00631451.
XX PR 15-SEP-2000; 2000US-00663870.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX DR WPI; 2001-476164/51.
XX DR N-PSDB; AAH99140.
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX PS Claim 20; Page 1269; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX SQ Sequence 45 AA;
Query Match 71.4%; Score 5; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQDYF 6
DB 22 SQDYF 26
RESULT 15
AAO08447
ID AAO08447 standard; protein; 52 AA.
XX AC AAO08447;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 22339.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AA188378.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX PS Claim 20; SEQ ID NO 22339; 1399pp + Sequence Listing; English.
XX CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 52 AA;
Query Match 71.4%; Score 5; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDY 5
DB 2 SSQDY 6

Search completed: November 7, 2005, 19:27:58
Job time : 7.02703 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:15:40 ; Search time 0.851351 Seconds
(without alignments)
791.116 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	478	JK0201	alpha-amylase (EC
2	7	100.0	498	A48305	alpha-amylase (EC
3	7	100.0	499	ALAS1	alpha-amylase (EC
4	7	100.0	499	ALAS3	alpha-amylase (EC
5	7	100.0	499	JS0663	alpha-amylase (EC
6	7	100.0	499	JT0466	alpha-amylase (EC
7	7	100.0	499	JN0588	alpha-amylase (EC
8	7	100.0	499	B48305	alpha-amylase (EC
9	7	100.0	624	JC4510	pullulanase (EC 3.
10	6	85.7	317	E84088	restriction endonu
11	6	85.7	351	E86187	YUP8H12.10 {import
12	5	71.4	104	E49803	hypothetical prote
13	5	71.4	129	H71046	hypothetical prote
14	5	71.4	144	JC7121	androgenic gland h
15	5	71.4	178	H96905	hypothetical prote
16	5	71.4	180	B95039	hypothetical prote
17	5	71.4	217	S61191	asymmetrical hydro
18	5	71.4	253	A05283	spectrin alpha cha
19	5	71.4	289	A43562	homeotic protein H
20	5	71.4	295	B84747	hypothetical prote
21	5	71.4	326	AF2082	iron(III) dicitrat
22	5	71.4	330	H75068	dipeptide abc tran
23	5	71.4	330	B71163	probable oligopept
24	5	71.4	331	T06227	peroxidase (EC 1.1
25	5	71.4	332	T10790	peroxidase (EC 1.1
26	5	71.4	420	T42616	envelope protein -
27	5	71.4	423	A12189	hypothetical prote
28	5	71.4	426	H71483	probable phosphat
29	5	71.4	459	H81324	probable MCP-domai

30	5	71.4	469	2	B90110	TATA box-binding p
31	5	71.4	482	2	A90248	conserved hypothet
32	5	71.4	486	2	AD0373	probable exported
33	5	71.4	547	2	S61032	hypothetical prote
34	5	71.4	551	1	JC5225	dsRNA-activated pr
35	5	71.4	569	2	C87598	TonB-dependent rec
36	5	71.4	675	2	B64646	polyposphate kina
37	5	71.4	675	2	F71935	polyposphate kina
38	5	71.4	813	2	I41292	EcOg type I restri
39	5	71.4	829	2	AC0776	probable outer mem
40	5	71.4	837	2	H87638	TonB-dependent rec
41	5	71.4	863	2	T47038	hypothetical prote
42	5	71.4	863	2	AD0234	probable fimbrial
43	5	71.4	943	2	T33795	hypothetical prote
44	5	71.4	1262	2	T30524	protein phosphatas
45	5	71.4	1564	2	S55517	probable transport

ALIGNMENTS

RESULT 1

JK0201

alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae

N:Alternate names: glycogenase; Taka-amylase A

C:Species: Aspergillus oryzae

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004

C:Accession: JK0201

R:Toda, H.; Kondo, K.; Narita, K.

Proc. Jpn. Acad. 58B, 208-212, 1982

A:Title: The complete amino acid sequence of Taka-amylase A.

A:Reference number: JK0201

A:Accession: JK0201

A:Molecule type: protein

A:Residues: 1-478 <TOD>

A:Cross-references: UNIPROT:P10529

C:Comment: One atom of calcium per molecule is essential for the activity.

C:Comment: This enzyme is a glycoprotein.

C:Comment: See also PIR:JT0466 and PIR:JS0240.

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation

F:173-300/Domain: alpha-amylase core homology <AMY>

F:197/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:210,230,297/Active site: His, Glu, Asp #status experimental

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 478;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSQDYFH 7

|||||

Db 141 SSQDYFH 147

RESULT 2

A48305

alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori

C:Species: Aspergillus awamori

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: A48305

R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;

Curr. Genet. 17, 203-212, 1990

A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe

A:Reference number: A48305; MUID:90254827; PMID:2340591

A:Accession: A48305

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-498 <KOR>

A:Cross-references: UNIPROT:Q02905

C:Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
 C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
 F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 7; DB 2; Length 498;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||

Db 162 SSQDYFH 168

RESULT 3

ALAS1

alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
 N;Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
 C;Species: Aspergillus oryzae
 C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
 C;Accession: S04548; A33214; J50240; A91930; A93767; A10627
 R;Wirsal, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
 Mol. Microbiol. 3, 3-14, 1989

A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c
 A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Accession: S04548

A;Molecule type: DNA

A;Residues: 1-499 <WIR>

A;Cross-references: UNIPROT:P10529; EMBL:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

A;Genetics: AMY1

A;Accession: A33214

A;Molecule type: mRNA

A;Residues: 1-499 <W12>

A;Cross-references: GB:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989

A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing

A;Reference number: JS0240; MUID:89378767; PMID:2789162

A;Accession: JS0240

A;Molecule type: DNA

A;Residues: 1-499 <GEN>

A;Genetics: AMY2

A;Note: the authors refer to this as isozyme II

R;Isemura, S.; Ikenaka, T.

J. Biochem. 74, 1-10, 1973

A;Reference number: A91930; MUID:74001521; PMID:4733850

A;Accession: A91930

A;Molecule type: protein

A;Residues: 206-225 <ISE>

R;Narita, K.

Proc. Jpn. Acad. 51, 285-290, 1975

A;Reference number: A93767

A;Accession: A93767

A;Molecule type: protein

A;Residues: 434-443, 446-447, 'Q', 449-458, 'GTVV', 459-464, 467-468, 'B', 470, 'B', 472-499 <NAR>

R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A;Title: Structure and possible catalytic residues of Taka-amylase A.

A;Reference number: A37454; MUID:84212370; PMID:6609921

A;Contents: annotation; X-ray crystallography, 3.0 angstroms

R;Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkmenburg, J.P.; Wilkinson, A.

submitted to the Brookhaven Protein Data Bank, August 1992

A;Reference number: A51548; PDB:6TAA

A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497

C;Comment: One atom of calcium per molecule is essential for activity.

C;Genetics: <AMY1>

A;Gene: amy1

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Genetics: <AMY2>

A;Gene: amy2; Amy11

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
 C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; poly
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-499/Product: alpha-amylase 1 #status experimental <MAT>
 F;194-321/Domain: alpha-amylase core homology <AMY>
 F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
 F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
 F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 7; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 0.35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||

Db 162 SSQDYFH 168

RESULT 4

ALAS3

alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae

N;Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A

C;Species: Aspergillus oryzae

C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004

C;Accession: S04549; A33215; A44713

R;Wirsal, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.

Mol. Microbiol. 3, 3-14, 1989

A;Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon c

A;Reference number: S04548; MUID:89237897; PMID:2785629

A;Accession: S04549

A;Molecule type: DNA

A;Residues: 1-499 <WIR>

A;Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922

A;Accession: A33215

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-499 <W12>

A;Cross-references: GB:X12727; NID:G2454; PIDN:CAA31220.1; PID:G295922

R;Genes, M.J.; Dove, M.J.; Seligy, V.L.

Gene 79, 107-117, 1989

A;Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containing

A;Reference number: JS0240; MUID:89378767; PMID:2789162

A;Accession: A44713

A;Molecule type: DNA

A;Residues: 1-499 <GEN>

A;Note: the authors refer to this as isozyme I

R;Matsuura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.

J. Biochem. 95, 697-702, 1984

A;Title: Structure and possible catalytic residues of Taka-amylase A.

A;Reference number: A37454; MUID:84212370; PMID:6609921

A;Contents: annotation; X-ray crystallography, 3.0 angstroms

C;Comment: One atom of calcium per molecule is essential for activity.

C;Genetics:

A;Gene: amy3; AmyI

A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; metal

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-499/Product: alpha-amylase 3 #status experimental <MAT>

F;194-321/Domain: alpha-amylase core homology <AMY>

F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental

F;142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted

F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 100.0%; Score 7; DB 1; Length 499;

Best Local Similarity 100.0%; Pred. No. 0.35;

```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 5
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C:Species: Aspergillus sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C:Accession: JS0663
R:Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A:Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyasamii and its expression
A:Reference number: JS0663; MUID:92323146; PMID:1368777
A:Accession: JS0663
A:Molecule type: mRNA
A:Residues: 1-499 <SHI>
A:Cross-references: UNIPROT:P10529
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <ALP>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 6
JT0466
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N:Alternate names: glycogenase; taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: JT0466
R:Tada, S.; Iimura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.
Agric. Biol. Chem. 53, 593-599, 1989
A:Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergillus
A:Reference number: JT0466
A:Accession: JT0466
A:Molecule type: DNA
A:Residues: 1-499 <TAD>
A:Cross-references: UNIPROT:P10529
C:Comment: See also PIR:JK0201 and PIR:JS0240.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:231,251,318/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 7
JN0588
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
N:Alternate names: Taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: JN0588
R:Tsuikagoshi, N.; Furukawa, M.; Nagaba, H.; Kiritani, N.; Tsuibo, A.; Uda, S.
Gene 84, 313-327, 1989
A:Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for m
A:Reference number: JN0588; MUID:90128276; PMID:2612911
A:Accession: JN0588
A:Molecule type: mRNA
A:Residues: 1-499 <TSU>
A:Cross-references: UNIPROT:Q96TH4
C:Comment: The alpha amylases are encoded by multigene family.
C:Genetics:
A:Gene: Taa-G1
A:Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase #status predicted <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 8
B48305
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: B48305
R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Aspe
A:Reference number: A48305; MUID:90254827; PMID:2340591
A:Accession: B48305
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499 <KOR>
A:Cross-references: UNIPROT:Q02906
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:194-321/Domain: alpha-amylase core homology <AMY>

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

```

RESULT 9

JC4510
pullulanase (EC 3.2.1.41) precursor - yeast (lipomyces kononenkoae)
N:Alternate names: LKAI protein; raw starch-degrading amylase
N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C:Species: lipomyces kononenkoae
C:Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4510; PC4116
R:Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a lipoc
A:Reference number: JC4510; MUID:96105202; PMID:8529895
A:Accession: JC4510
A:Molecule type: mRNA
A:Residues: 1-624 <STE>
A:Cross-references: UNIPROT:Q01117; GB:U03076; NID:g1173536; PIDN:AAC49622.1; PID:g11735
A:Experimental source: strain IGC4052B
A:Accession: PC4116
A:Molecule type: protein
A:Residues: 29-44 <ST2>
A:Experimental source: IGC4052B
C:Genetics:
A:Gene: LKAI
C:Function:
A:Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
A:Pathway: glycogen/starch degradation
C:Superfamily: lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-624/Product: alpha-amylase #status predicted <MAT>
F:48-141/Domain: glucoamylase starch-binding domain homology <SBD>
F:320-447/Domain: alpha-amylase core homology <AMY>
F:177-185,297-311,387-430,587-622/Diulfide bonds: #status predicted
F:304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 100.0%; Score 7; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7

|||||
Db 288 SSQDYFH 294

RESULT 10

E84088
restriction endonuclease (HaeIII) BH3509 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: E84088
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: E84088
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-317 <STO>
A:Cross-references: UNIPROT:Q9K764; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB072
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3509

Query Match 85.7%; Score 6; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6

|||||
Db 142 SSQDYF 147

RESULT 11

E86187
YUP8H12.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86187
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 818-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Iuro, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86187
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-351 <STO>
A:Cross-references: UNIPROT:Q23041; GB:AE005172; NID:g2388568; PIDN:AAB71449.1; GSPDB:G
C:Genetics:
A:Map position: 1

Query Match 85.7%; Score 6; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6

|||||
Db 226 SSQDYF 231

RESULT 12

S49803
hypothetical protein YML058w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YM9958.04
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: S49803
R:Devlin, K.; Church, C.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49800
A:Accession: S49803
A:Molecule type: DNA
A:Residues: 1-104 <DEV>
A:Cross-references: UNIPROT:Q04964; EMBL:Z46729; NID:g577134; PIDN:CAA86717.1; PID:g5771
C:Genetics:
A:Gene: SGD:SMU1; MIPS:YML058w
A:Cross-references: SGD:S0004523
A:Map position: 13L
C:Superfamily: Saccharomyces hypothetical protein YML058w

Query Match 71.4%; Score 5; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYF 6

|||||
Db 4 SQDYF 8

RESULT 13

H71046
hypothetical protein PH1664 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: H71046
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: H71046
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-129 <KAW>
 A:Cross-references: UNIPROT:O59337; GB:AP000006; NID:G3236133; PIDN:BAA30776.1; PID:G325
 A:Experimental source: strain O13
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1664

Query Match 71.4%; Score 5; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDY 5
 |||||
 DB 29 SSQDY 33

RESULT 14

JC7121
 androgenic gland hormone precursor - common pill bug
 C:Species: Armadillidium vulgare (common pill bug)
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: JC7121
 R:Okuno, A.; Hasegawa, Y.; Ohira, T.; Katakura, Y.; Nagasawa, H.
 Biochem. Biophys. Res. Commun. 264, 419-423, 1999
 A:Title: Characterization and cDNA cloning of androgenic gland hormone of the terrestrial
 A:Reference number: JC7121; MUID:20001935; PMID:10529379
 A:Accession: JC7121
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-144 <OKU>
 A:Cross-references: UNIPROT:Q5U8R2; DBJ:AB029615; GB:AB029615; NID:G6446571; PID:G64465
 A:Experimental source: androgenic gland

Query Match 71.4%; Score 5; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
 |||||
 DB 82 QDYFH 86

RESULT 15

H96905
 hypothetical protein CAC0048 [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: H96905
 R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: H96905
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-178 <KUR>
 A:Cross-references: UNIPROT:Q97M21; GB:AE001437; PIDN:AAK78035.1; PID:gl5022870; GSPDB:G
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC0048

Query Match 71.4%; Score 5; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDY 5
 |||||

Db 34 SSQDY 38

Search completed: November 7, 2005, 19:33:48
Job time : 1.85135 secs

It's the way
the world is

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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:00:20 ; Search time 3.71622 Seconds
(without alignments)
964.571 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	7	100.0	498 1	AMYA ASPAW
2	7	100.0	498 2	Q76CT3
3	7	100.0	499 1	AMYA ASPOR
4	7	100.0	499 1	AMYB ASPAW
5	7	100.0	499 1	AMY APSH
6	7	100.0	499 2	Q96TH4
7	7	100.0	499 2	Q76LJ9
8	7	100.0	499 2	Q71V45
9	7	100.0	624 1	AMY1_LIPKO
10	7	100.0	647 2	Q6VF33
11	6	85.7	183 2	Q8D239
12	6	85.7	183 2	Q8E4P7
13	6	85.7	261 2	Q73L56
14	6	85.7	295 2	Q6CUI2
15	6	85.7	317 2	Q9K764
16	6	85.7	351 2	Q23041
17	5	71.4	49 2	Q6XYZ7
18	5	71.4	72 2	Q6TQU2
19	5	71.4	87 2	Q76LJ9
20	5	71.4	97 2	Q8M2M1
21	5	71.4	98 2	Q677E1
22	5	71.4	104 1	SML1_YEAST
23	5	71.4	119 2	Q7VQH5
24	5	71.4	125 2	Q751X1
25	5	71.4	129 2	Q59337
26	5	71.4	144 1	AGH ARMVU
27	5	71.4	163 2	Q73Q16
28	5	71.4	174 2	Q73Q16
29	5	71.4	177 2	Q7S6B6
30	5	71.4	178 2	Q97M21
31	5	71.4	180 2	Q97SK2

32	5	71.4	181	2	Q6IIG1	O6iig1 drosophila
33	5	71.4	185	2	Q8E118	Q8e118 streptococc
34	5	71.4	199	1	TDX TRYBR	Q26695 trypanosoma
35	5	71.4	199	2	Q71RY2	Q71ry2 trypanosoma
36	5	71.4	199	2	Q71SQ4	Q71sq4 trypanosoma
37	5	71.4	205	2	Q9U4F2	Q9u4f2 hydra atten
38	5	71.4	215	2	P97975	P97975 unidentified
39	5	71.4	217	1	HMT2_YEAST	P49775 saccharomyc
40	5	71.4	218	2	Q9CUH8	Q9cuH8 mus musculu
41	5	71.4	222	2	Q6ZUW9	Q6zuu9 homo sapien
42	5	71.4	224	2	Q70BE3	Q70be3 pseudomonas
43	5	71.4	237	2	Q7M8C0	Q7m8c0 wolinnella s
44	5	71.4	248	2	Q7YSZ6	Q7ysz6 rhodnius pr
45	5	71.4	253	2	Q8EUT6	Q8eut6 mycoplasma

ALIGNMENTS

RESULT 1
AMYA ASPAW
ID AMYA ASPAW STANDARD; PRT; 498 AA.
AC Q02905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amyase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase A).
GN Name=AMVA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amyase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X52755; CAA36966.1; --
CC PIR; A48305; A48305.
CC HSP; P10529; 7TAA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alp_amy1_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; Alpha-amyase; 1.
CC PRINTS; PR00110; ALPHAAMYASE.
CC SMART; SM00642; Amy; 1.
CC Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydroxylase; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 498 Alpha-amyase A.
FT ACT_SITE 27 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).

```

FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT METAL 196 196 similarity).
FT METAL 227 227 Calcium 1 (By similarity).
FT METAL 231 231 Calcium 2 (By similarity).
FT METAL 251 251 Calcium 1 (via carbonyl oxygen) (By
FT METAL 251 251 similarity).
FT METAL 51 59 Calcium 2 (By similarity).
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 498 AA; 54880 MW; 7659511BC01A8A01 CRC64;

Query Match 100.0%; Score 7; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 2
Q76CT3 PRELIMINARY; PRT; 498 AA.
AC Q76CT3
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Alpha-amylase.
GN Name=amyA;
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RA Ito K.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB109452; BAD01051.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHA-AMYLASE.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7F4E3FC0 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 3
AMYA_ASPOR STANDARD; PRT; 499 AA.
ID AMYA_ASPOR
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
DE alpha-D-glucan glucanohydrolase).
GN Name=AMY1;
GN and
GN Name=AMY2;

```

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GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RC MEDLINE=89237897; PubMed=2785629;
RX MEDLINE=89237897; PubMed=2785629;
RA Wiersel S., Lachmund A., Wildhardt G., Rutkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RT Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Uda S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";
RL J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzozowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.

```


CC -1- COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.
CC -1- SUBUNIT: Monomer.
CC -1- BIOTECHNOLOGY: Used in the brewing industry to increase the
CC fermentability of beer worts (including those made from unmalted
CC cereals), in the starch industry to make high maltose and high DE
CC syrups (starch saccharification), in the alcohol industry to
CC reduce fermentation time, in the cereal food industry for flour
CC supplementation and improvement of chilled and frozen dough, and
CC in the forestry industry for low-temperature modification of
CC starch. Sold under the name Fungamyl by Novozymes.
CC -1- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC -----
CC EMBL; X12725; CAA31218.1; -
CC EMBL; X12726; CAA31219.1; -
CC EMBL; X12727; CAA31220.1; -
CC EMBL; D00434; BAA00336.1; -
CC EMBL; M33218; AAA32708.1; -
CC PIR; JKO201; JKO201.
CC PIR; JTO466; JTO466.
CC PIR; S04548; ALAS1.
CC PDB; 2TAA; X-ray; A=22-499.
CC PDB; 6TAA; X-ray; @=22-499.
CC PDB; 7TAA; X-ray; @=22-499.
CC GlycoSuiteDB; P10529; -
CC InterPro: IPR006589; Alp_amy1_cat_sub.
CC InterPro: IPR006047; Alpha_amy1_cat.
CC InterPro: IPR006046; Glyco_hydro_13.
CC Pfam: PF00128; Alpha-amy1ase; 1.
CC PRINTS; PR00110; ALPHA-AMY1ASE.
CC SMART; SM00642; Amy; 1.
CC 3D-structure; Calcium-binding; Carbohydrate metabolism;
CC Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
CC Multigene family; Signal.
CC SIGNAL 1 21
CC CHAIN 22 499 Alpha-amy1ase A.
CC ACT_SITE 227 227 Nucleophile.
CC ACT_SITE 251 251 Proton donor.
CC ACT_SITE 318 318
CC METAL 142 142 Calcium 1.
CC METAL 183 183 Calcium 1 (via carbonyl oxygen).
CC METAL 196 196 Calcium 1.
CC METAL 227 227 Calcium 2.
CC METAL 231 231 Calcium 1 (via carbonyl oxygen).
CC METAL 251 251 Calcium 2.
CC DISULFID 51 59
CC DISULFID 171 185
CC DISULFID 261 304
CC DISULFID 461 496
CC CARBOHYD 218 218 N-linked (GlcNAc...)/FTID-CAR 000125.
CC VARIANT 56 56 Q -> R (in AMY3).
CC VARIANT 172 172 F -> L (in AMY3).
CC CONFLICT 93 94 TT -> DC (in Ref. 5).
CC CONFLICT 106 106 D -> T (in Ref. 5).
CC CONFLICT 184 184 D -> Y (in Ref. 3).
CC CONFLICT 195 195 P -> L (in Ref. 3).
CC CONFLICT 255 255 D -> V (in Ref. 3).
CC CONFLICT 291 291 D -> H (in Ref. 4).
CC CONFLICT 345 345 I -> L (in Ref. 5).
CC CONFLICT 370 370 L -> A (in Ref. 4).
CC CONFLICT 406 409 WPY -> PYI (in Ref. 5).
CC CONFLICT 448 448 G -> S (in Ref. 5).
CC CONFLICT 497 497 S -> SD (in Ref. 5 and 7).

FT HELIX 24 27
FT TURN 28 29
FT STRAND 32 35
FT HELIX 37 40
FT STRAND 42 42
FT TURN 43 44
FT HELIX 53 55
FT STRAND 61 61
FT HELIX 63 68
FT TURN 69 69
FT HELIX 70 74
FT TURN 75 77
FT STRAND 80 83
FT STRAND 87 89
FT STRAND 94 94
FT TURN 95 96
FT STRAND 97 97
FT TURN 100 101
FT STRAND 105 111
FT TURN 113 114
FT HELIX 118 130
FT TURN 131 132
FT STRAND 134 139
FT STRAND 143 143
FT STRAND 146 148
FT HELIX 150 152
FT STRAND 155 157
FT STRAND 159 159
FT HELIX 164 166
FT STRAND 167 167
FT TURN 176 177
FT STRAND 179 184
FT STRAND 186 188
FT STRAND 192 194
FT STRAND 196 197
FT TURN 199 200
FT HELIX 202 219
FT TURN 220 220
FT STRAND 223 226
FT HELIX 229 231
FT TURN 234 235
FT HELIX 236 244
FT TURN 245 245

Query Match 100.0%; Score 7; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

RESULT 4
AMYB ASPAW
ID AMYB ASPAW STANDARD; PRT; 499 AA.
AC Q02906;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amy1ase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase B).
GN Name=AMYB;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,

RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
 RT "Cloning, characterization, and expression of two alpha-amylase genes
 from *Aspergillus niger* var. *awamori*.",
 RL Curr. Genet. 17:203-212(1990).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 at high concentrations (By similarity).
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC
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 CC EMBL; X52756; CAA36967.1; -.
 DR PIR; B48305; B48305.
 DR HSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Multigene family; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 499
 FT ACT_SITE 227 227
 FT ACT_SITE 251 251
 FT ACT_SITE 318 318
 FT METAL 142 142
 FT METAL 183 183
 FT METAL 196 196
 FT METAL 227 227
 FT METAL 231 231
 FT METAL 251 251
 FT DISULFID 51 59
 FT DISULFID 171 185
 FT DISULFID 261 304
 FT DISULFID 461 496
 FT CARBOHYD 218 218
 SQ SEQUENCE 499 AA; 54921 MW; 740B96B11BC01A8A CRC64;

Query Match 100.0%; Score 7; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 162 SSQDYFH 168

RESULT 5

AMY ASPSH STANDARD; PRT; 499 AA.
 AC P30292.
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 glucanohydrolase).
 DE Name=AMY;
 OS *Aspergillus shiroyamae*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5070;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=92323146; PubMed=1368777;
 RA Shibuya I., Tamura G., Ishikawa T., Hara S.;
 RT "Cloning of the alpha-amylase cDNA of *Aspergillus shiroyamae* and its
 expression in *Saccharomyces cerevisiae*.",
 RL Biochem. Biotechnol. Biochem. 56:174-179(1992).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 at high concentrations (By similarity).
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D10461; BAA01255.1; -.
 DR HSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 499
 FT ACT_SITE 227 227
 FT ACT_SITE 251 251
 FT ACT_SITE 318 318
 FT METAL 142 142
 FT METAL 183 183
 FT METAL 196 196
 FT METAL 227 227
 FT METAL 231 231
 FT METAL 251 251
 FT DISULFID 51 59
 FT DISULFID 171 185
 FT DISULFID 261 304
 FT DISULFID 461 496
 FT CARBOHYD 218 218
 SQ SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;

Query Match 100.0%; Score 7; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db 162 SSQDYFH 168

RESULT 6

Q96TH4 PRELIMINARY; PRT; 499 AA.
 AC Q96TH4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Taka-amylase A (EC 3.2.1.1).
 DE Name=amyA;
 OS *Aspergillus oryzae*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; *Aspergillus*.
 OX NCBI_TaxID=5062;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=RIB40;
RX MEDLINE=20289310; PubMed=10830498;
RA Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
RT gene, amyR, involved in the amylolytic gene expression in Aspergillus
RT oryzae.";
RL Biosci. Biotechnol. Biochem. 64:816-827(2000).
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB021876; BAA95703.1; -.
DR PIR; JN0588; JN0588.
DR PIR; S04549; ALAS3.
DR HSSP; P10529; 7TAA.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha.amyl.cat.
DR InterPro; IPR006589; Alp.amyl.cat.sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

RESULT 7
Q76L99 PRELIMINARY; PRT; 499 AA.
ID Q76L99;
AC Q76L99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase precursor.
GN Name=amyI;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB083159; BAD06002.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha.amyl.cat.
DR InterPro; IPR006589; Alp.amyl.cat.sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

RESULT 8
Q7LV45 PRELIMINARY; PRT; 499 AA.
ID Q7LV45;
AC Q7LV45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN Name=amyI;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5059;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=86-10D;
RA Fakhoury A.M., Woloshuk C.P.;
RT "AmyI, the alpha-amylase gene of Aspergillus flavus: Involvement in
RT aflatoxin biosynthesis in maize kernels.";
RL Phytopathology 89:908-914(1999).
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AF139925; AAF14264.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha.amyl.cat.
DR InterPro; IPR006589; Alp.amyl.cat.sub.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EEF42ADA71D20DA9 CRC64;

Query Match 100.0%; Score 7; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
DB 162 SSQDYFH 168

RESULT 9
AMY1_LIPKO
ID AMY1_LIPKO STANDARD; PRT; 624 AA.
AC Q01117;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase 1).
GN Name=LKA1;
OS Lipomyces kononenkoae.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Lipomycetaceae; Lipomyces.
OX NCBI_TaxID=34357;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IGC4052B;
RX MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;
RA Steyn A.J.C., Marmur J., Pretorius I.S.;
RT "Cloning, sequence analysis and expression in yeasts of a cDNA
RT containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";
RL Gene 166:65-71(1995).
RN [2]
RP SEQUENCE OF 29-44.
RC STRAIN=IGC4052B;
RX MEDLINE=96132108; PubMed=8593683;
RA Steyn A.J.C., Pretorius I.S.;
```

RT "Characterization of a novel alpha-amylase from *Lipomyces kononenkoae*
 RL and expression of its gene (LKAL1) in *Saccharomyces cerevisiae*.";
 CC Curr. Genet. 28:526-533 (1995).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
 CC at high concentrations (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -1- SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
 CC domain.
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 CC -----
 DR EMBL; U30376; AAC49622.1; ALT_INIT.
 DR FIR; JC4510; JC4510.
 DR HSP; F10529; 7TAA.
 DR InterPro; IPR006589; Alp_aml_cat_sub.
 DR InterPro; IPR006047; Alpha_aml_cat.
 DR InterPro; IPR005036; CBM 21.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR Pfam; PF03370; CBM 21; 1.
 DR SMART; SM00642; Amy; 1.
 DR Calcium-binding; Carbohydrate metabolism; Direct protein sequencing;
 KW Glycoprotein; Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 624
 FT DOMAIN 40 133
 FT ACT_SITE 353 353
 FT ACT_SITE 377 377
 FT ACT_SITE 444 444
 FT METAL 268 268
 FT METAL 309 309
 FT METAL 322 322
 FT METAL 353 353
 FT METAL 357 357
 FT METAL 377 377
 FT DISULFID 177 185
 FT DISULFID 297 311
 FT DISULFID 387 430
 FT DISULFID 587 622
 FT CARBOHYD 304 304
 FT CARBOHYD 344 344
 SQ SEQUENCE 624 AA; 58876 MW; 87EB16534F5A9A9F CRC64;
 Query Match 100.0%; Score 7; DB 1; Length 624;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 7
 DB 288 SSQDYFH 294
 RESULT 10
 Q6YF33 PRELIMINARY; PRT; 647 AA.
 AC Q6YF33
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Alpha-amylase.
 OS *Lipomyces starkeyi*.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Lipomycetaceae; Lipomycetes.

OX NCBI_TaxID=29829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KSM 22W;
 RX PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
 RA Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
 RA Moon T.-W.;
 RT "Cloning and expression of *Lipomyces starkeyi* alpha-amylase in
 RT *Escherichia coli* and determination of some of its properties.";
 RL FEMS Microbiol. Lett. 233:53-64 (2004).
 DR EMBL; AY15463; AAN75021.1; -.
 DR HSP; P26827; 1A47.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_aml_cat.
 DR InterPro; IPR006589; Alp_aml_cat_sub.
 DR InterPro; IPR005036; CBM 21.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR Pfam; PF03370; CBM 21; 1.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;
 Query Match 100.0%; Score 7; DB 2; Length 647;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 7
 DB 311 SSQDYFH 317
 RESULT 11
 Q8DZ39 PRELIMINARY; PRT; 183 AA.
 ID Q8DZ39
 AC Q8DZ39
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein SAG1281.
 GN OrderedLocustNames=SAG1281;
 OS *Streptococcus agalactiae* (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC *Streptococcus*.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
 RA Tettelin H., Masiagnani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Iacobino E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
 RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V *Streptococcus agalactiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
 DR EMBL; AE014250; AAN00154.1; -.
 DR TIGR; SAG1281; -.
 KW Complete proteome.
 SQ SEQUENCE 183 AA; 21278 MW; 029AD020DF762720 CRC64;
 Query Match 85.7%; Score 6; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SSQDYFH 6
 DB 135 SSQDYFH 140

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RESULT 12
Q8E4P7
ID Q8E4P7 PRELIMINARY; PRT; 183 AA.
AC Q8E4P7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein gba1354.
GN OrderedLocusNames=gsa1354;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=224242508; PubMed=12354221;
RA Glaser P., Rueniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease";
RL Mol. Microbiol. 45:1499-1513 (2002).
DR EMBL; AL766850; CAD47013.1; -.
DR Sagalish; gba1354; -.
KW Complete proteome.
SQ SEQUENCE 183 AA; 21243 MW; 12A79C080C813D5C CRC64;

Query Match 85.7%; Score 6; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6
Db 135 SSQDYF 140

RESULT 13
Q73L56
ID Q73L56 PRELIMINARY; PRT; 261 AA.
AC Q73L56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TFD2009;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Sedadri R., Myers G.S.A., Tettelin H., Bisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidgen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajls D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
DR EMBL; AE017252; AA012523.1; -.
DR TIGR; TDE2009; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR PROSITE; PS00030; RRM_RNF_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 30170 MW; 7F11DC42F0894499 CRC64;

Query Match 85.7%; Score 6; DB 2; Length 261;

Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6
Db 123 SSQDYF 128

RESULT 14
Q6CUY2
ID Q6CUY2 PRELIMINARY; PRT; 295 AA.
AC Q6CUY2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y-
DE 1140 of Kluyveromyces lactis.
GN ORFNames=KLLA0C013869;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrains A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RC STRAIN=NRRL Y-1140;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382123; CAH01108.1; -.
DR GO; GO:0007163; P:signal transduction; IEA.
DR InterPro; IPR001593; RA.
DR InterPro; IPR010993; SAM_homology.
DR Pfam; PF00788; RA; 1.
DR SMART; SM00314; RA; 1.
DR PROSITE; PS02000; RA; 1.
SQ SEQUENCE 295 AA; 32546 MW; E6A28199F8830A06 CRC64;

Query Match 85.7%; Score 6; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYF 6
Db 138 SSQDYF 143

RESULT 15
Q9K764
ID Q9K764 PRELIMINARY; PRT; 317 AA.
AC Q9K764;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Restriction endonuclease (HaeIII).

```

GN OrderedLocusNames=BH3509;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001519; BAB07228.1; -.
DR PIR; E84088; E84088.
DR GO; GO:0004519; F:endonuclease activity; IEA.
KW Complete proteome; Endonuclease.
SQ SEQUENCE 317 AA; 36616 MW; 0860B7466391DC72 CRC64;

Query Match 85.7%; Score 6; DB 2; Length 317;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSQDYF 6
Db 142 SSQDYF 147
|||||

Search completed: November 7, 2005, 19:32:41
Job time : 5.71622 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:45:18 ; Search time 1.05405 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	478	1	US-08-720-899-7
2	7	100.0	478	1	US-08-459-610-7
3	7	100.0	478	2	US-08-343-804-7
4	7	100.0	478	2	US-08-339-715A-2
5	7	100.0	478	2	US-08-600-908A-10
6	7	100.0	478	3	US-08-683-838A-10
7	7	100.0	478	3	US-09-182-859-7
8	7	100.0	478	4	US-09-672-459-7
9	7	100.0	478	4	US-09-636-252A-10
10	7	100.0	478	4	US-10-186-042-7
11	5	71.4	84	4	US-09-583-110-4016
12	5	71.4	95	4	US-09-107-433-4442
13	5	71.4	113	4	US-09-248-796A-14523
14	5	71.4	153	4	US-09-369-247-166
15	5	71.4	153	4	US-09-270-767-47564
16	5	71.4	154	4	US-09-369-247-108
17	5	71.4	180	4	US-09-248-796A-22820
18	5	71.4	187	4	US-09-248-796A-19796
19	5	71.4	191	4	US-09-248-796A-22814
20	5	71.4	203	2	US-08-598-873-4
21	5	71.4	203	3	US-08-605-430-4
22	5	71.4	203	4	US-09-717-054-4
23	5	71.4	206	4	US-09-902-540-12425
24	5	71.4	210	4	US-09-248-796A-19369
25	5	71.4	303	4	US-09-328-352-5164
26	5	71.4	317	4	US-09-107-532A-4653
27	5	71.4	450	4	US-09-369-247-97

28	5	71.4	508	4	US-09-369-247-167	Sequence 167, App
29	5	71.4	550	1	US-08-143-219-25	Sequence 25, Appl
30	5	71.4	551	2	US-08-436-771-9	Sequence 9, Appli
31	5	71.4	551	2	US-08-434-998-9	Sequence 9, Appli
32	5	71.4	551	2	US-08-487-797-9	Sequence 9, Appli
33	5	71.4	551	4	US-09-949-016-6268	Sequence 6268, Ap
34	5	71.4	551	5	PCT-US95-02088-9	Sequence 9, Appli
35	5	71.4	577	4	US-09-248-796A-19304	Sequence 19304, A
36	5	71.4	590	4	US-09-248-796A-26874	Sequence 26874, A
37	5	71.4	591	4	US-09-949-016-11452	Sequence 11452, A
38	5	71.4	784	3	US-09-371-913A-7	Sequence 7, Appli
39	5	71.4	784	4	US-09-967-805-7	Sequence 7, Appli
40	5	71.4	788	4	US-09-107-532A-6538	Sequence 6538, Ap
41	5	71.4	792	4	US-09-134-000C-5895	Sequence 5895, Ap
42	5	71.4	974	4	US-09-252-991A-23640	Sequence 23640, A
43	5	71.4	998	4	US-09-252-991A-28424	Sequence 28424, A
44	5	71.4	1118	4	US-09-949-016-6596	Sequence 6596, Ap
45	5	71.4	1120	4	US-09-949-016-10404	Sequence 10404, A

ALIGNMENTS

RESULT 1
US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 57534600 No. 5753460disk of No. 5753460ch America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-720-899-7

Query Match 100.0%; Score 7; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SSQDYFH 7
Db      141 SSQDYFH 147

RESULT 2
US-08-459-610-7
; Sequence 7, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. 5801043o No. 5801043disk of No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-459-610-7

Query Match      100.0%; Score 7; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
Db      141 SSQDYFH 147

RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: JP 306096/1993
```

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; ADDRESSSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-343-804-7

Query Match      100.0%; Score 7; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
Db      141 SSQDYFH 147

RESULT 4
US-08-339-715A-2
; Sequence 2, Application US/08339715A
; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriaki, Takashi
; APPLICANT: Yanase, Michiyo
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: JP 306096/1993
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; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiser, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-339-715A-2

Query Match 100.0%; Score 7; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 5
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-600-908A-10

Query Match 100.0%; Score 7; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 7
US-09-182-859-7
; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisg rd-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER FILING DATE: 1996-04-30
; EARLIER FILING DATE: 1996-04-30
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; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7
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Query Match 100.0%; Score 7; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
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RESULT 8
US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7
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Query Match 100.0%; Score 7; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
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RESULT 9
US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
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; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10
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Query Match 100.0%; Score 7; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
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RESULT 10
US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7
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Query Match 100.0%; Score 7; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147
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RESULT 11
US-09-583-110-4016
; Sequence 4016, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
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; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4016
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4016

Query Match 71.4%; Score 5; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
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Db 40 QDYFH 44

RESULT 12
US-107-433-4442

; Sequence 4442, Application US/09107433
; Patent No. 6800744

GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 5206

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: <Unknown>

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,433

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/ 085131

; FILING DATE: May 12, 1998

; APPLICATION NUMBER: 60/051553

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-011

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 4442:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 95 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: Streptococcus pneumoniae

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...95

; SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

US-09-107-433-4442

Query Match 71.4%; Score 5; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDYFH 7
|||||
Db 51 QDYFH 55

RESULT 13

US-09-248-796A-14523

; Sequence 14523, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 14523

; LENGTH: 113

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-14523

Query Match 71.4%; Score 5; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYF 6
|||||
Db 43 SQDYF 47

RESULT 14

US-09-369-247-166

; Sequence 166, Application US/09369247

; Patent No. 6569992

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 44 Human Secreted Proteins

; FILE REFERENCE: P2024P1

; CURRENT APPLICATION NUMBER: US/09/369,247

; CURRENT FILING DATE: 1999-08-05

; EARLIER APPLICATION NUMBER: 60/074,118

; EARLIER FILING DATE: 1998-02-09

; EARLIER APPLICATION NUMBER: 60/074,157

; EARLIER FILING DATE: 1998-02-09

; EARLIER APPLICATION NUMBER: 60/074,137

; EARLIER FILING DATE: 1998-02-09

; EARLIER APPLICATION NUMBER: 60/074,341

; EARLIER FILING DATE: 1998-02-09

; EARLIER APPLICATION NUMBER: 60/074,141

; EARLIER FILING DATE: 1998-02-09

; NUMBER OF SEQ ID NOS: 172

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 166

; LENGTH: 153

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-369-247-166

Query Match 71.4%; Score 5; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQDYF 6

Db 124 SQDYF 128

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RESULT 15
US-09-270-767-47564
; Sequence 47564, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47564
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47564

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Query Match 71.4%; Score 5; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 SQDYF 6
Db 1 SQDYF 5

Search completed: November 7, 2005, 19:00:10
Job time : 2.05405 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:04 ; Search time 3.74324 Seconds
(without alignments)
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Title: US-10-820-200-2_COPY_161_167

Perfect score: 7

Sequence: 1 SSQDYFH 7

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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7	100.0	476	17	US-10-877-849-43
2	7	100.0	478	14	US-10-186-771-10
3	7	100.0	478	14	US-10-186-042-7
4	7	100.0	478	15	US-10-644-187-7
5	7	100.0	478	17	US-10-926-720-10
6	7	100.0	478	17	US-10-980-759-7
7	7	100.0	478	20	US-11-064-196-10
8	7	100.0	498	16	US-10-815-495-22
9	7	100.0	498	16	US-10-820-200-2
10	7	100.0	498	17	US-10-877-849-30
11	7	100.0	499	16	US-10-815-495-18

12	7	100.0	499	16	US-10-797-393A-5	Sequence 5, Appli
13	7	100.0	608	17	US-10-877-849-40	Sequence 40, Appl
14	7	100.0	640	17	US-10-877-849-36	Sequence 36, Appl
15	7	100.0	1095	14	US-10-228-063-45	Sequence 45, Appl
16	5	71.4	55	16	US-10-425-115-307711	Sequence 307711,
17	5	71.4	59	16	US-10-425-115-325770	Sequence 325770,
18	5	71.4	60	15	US-10-424-599-212201	Sequence 212201,
19	5	71.4	61	15	US-10-424-599-153435	Sequence 153435,
20	5	71.4	65	16	US-10-425-115-281545	Sequence 281545,
21	5	71.4	73	16	US-10-437-963-182457	Sequence 182457,
22	5	71.4	82	15	US-10-424-599-162468	Sequence 162468,
23	5	71.4	82	15	US-10-424-599-164927	Sequence 164927,
24	5	71.4	82	16	US-10-437-963-113292	Sequence 113292,
25	5	71.4	86	16	US-10-425-115-355307	Sequence 355307,
26	5	71.4	89	16	US-10-425-115-287848	Sequence 287848,
27	5	71.4	92	15	US-10-424-599-226734	Sequence 226734,
28	5	71.4	94	20	US-11-097-143-41466	Sequence 41466, A
29	5	71.4	95	18	US-10-617-320-4442	Sequence 4442, Ap
30	5	71.4	104	9	US-09-814-661A-2	Sequence 2, Appli
31	5	71.4	110	16	US-10-437-963-123791	Sequence 123791,
32	5	71.4	116	16	US-10-767-701-33822	Sequence 33822, A
33	5	71.4	119	15	US-10-424-599-155789	Sequence 155789,
34	5	71.4	126	16	US-10-425-115-319361	Sequence 319361,
35	5	71.4	134	18	US-10-773-236-387	Sequence 387, App
36	5	71.4	152	16	US-10-425-115-271310	Sequence 271310,
37	5	71.4	153	14	US-10-082-548-166	Sequence 166, App
38	5	71.4	153	17	US-10-918-446-166	Sequence 166, App
39	5	71.4	153	19	US-11-002-755-166	Sequence 166, App
40	5	71.4	153	20	US-11-002-756-166	Sequence 166, App
41	5	71.4	154	14	US-10-062-548-108	Sequence 108, App
42	5	71.4	154	17	US-10-918-446-108	Sequence 108, App
43	5	71.4	154	19	US-11-002-755-108	Sequence 108, App
44	5	71.4	154	20	US-11-002-756-108	Sequence 108, App
45	5	71.4	171	15	US-10-424-599-169013	Sequence 169013,

ALIGNMENTS

RESULT 1
US-10-877-849-43
; Sequence 43, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

Query Match 100.0%; Score 7; DB 17; Length 476;

Best Local Similarity 100.0%; Pred. No. 2.7; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 2
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match 100.0%; Score 7; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 3
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 100.0%; Score 7; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 4
US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match 100.0%; Score 7; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 5
US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475

REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 100.0%; Score 7; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 6

US-10-980-759-7
Sequence 7, Application US/10980759
Publication No. US20050118695A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/980,759
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US/09/672,459
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 478
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-980-759-7

Query Match 100.0%; Score 7; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 7

US-11-064-196-10
Sequence 10, Application US/11064196
Publication No. US20050170487A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants

FILE REFERENCE: 0776/11216-US2
CURRENT APPLICATION NUMBER: US/11/064,196
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: US/09/636,252
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 478
TYPE: PRT
ORGANISM: A. oryzae
US-11-064-196-10

Query Match 100.0%; Score 7; DB 20; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 8

US-10-815-495-22
Sequence 22, Application US/10815495
Publication No. US20040191864A1
GENERAL INFORMATION:
APPLICANT: Novozymes Biotech, Inc.
APPLICANT: Connelly, Mariah
APPLICANT: Brody, Howard
TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
FILE REFERENCE: 10345.200-US
CURRENT APPLICATION NUMBER: US/10/815,495
CURRENT FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 498
TYPE: PRT
ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 100.0%; Score 7; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 9

US-10-820-200-2
Sequence 2, Application US/10820200
Publication No. US20040229764A1
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Pedersen, Sven
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
FILE REFERENCE: 5835.200-US
CURRENT APPLICATION NUMBER: US/10/820,200
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US/09/710,339
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/165,786
PRIOR FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2

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; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match      100.0%; Score 7; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 10
US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match      100.0%; Score 7; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 11
US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connolly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match      100.0%; Score 7; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167
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Db 162 SSQDYFH 168

RESULT 12
US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Festeren, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match      100.0%; Score 7; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 162 SSQDYFH 168

RESULT 13
US-10-877-849-40
; Sequence 40, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 40
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-40

Query Match      100.0%; Score 7; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 14
US-10-877-849-36
; Sequence 36, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
```


; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikso-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial
US-10-877-849-36

Query Match 100.0%; Score 7; DB 17; Length 640;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 161 SSQDYFH 167

RESULT 15
US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shirousami
US-10-228-063-45

Query Match 100.0%; Score 7; DB 14; Length 1095;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

Search completed: November 7, 2005, 19:22:50
Job time : 3.74324 secs

Large Blackberry

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:04 ; Search time 266.305 Seconds
(without alignments)
782.441 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1867879 seqs, 418409474 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	498	100.0	498	16	US-10-820-200-2
2	498	100.0	498	16	US-10-877-849-30
3	498	100.0	499	16	US-10-797-393A-5
4	498	100.0	608	17	US-10-877-849-40
5	498	100.0	640	17	US-10-877-849-36
6	476	95.6	476	17	US-10-877-849-43
7	391	78.5	478	14	US-10-184-771-10
8	391	78.5	478	14	US-10-186-042-7
9	391	78.5	478	15	US-10-644-187-7
10	391	78.5	478	17	US-10-926-720-10
11	391	78.5	478	17	US-10-980-759-7

12	391	78.5	478	20	US-11-064-196-10	Sequence 10, Appl
13	384	77.1	498	16	US-10-815-495-22	Sequence 22, Appl
14	384	77.1	499	16	US-10-815-495-18	Sequence 18, Appl
15	377	75.7	1095	14	US-10-238-063-45	Sequence 45, Appl
16	23	4.6	495	14	US-10-213-990-42	Sequence 42, Appl
17	20	4.0	494	17	US-10-486-868-13	Sequence 13, Appl
18	19	3.8	513	15	US-10-389-493-2223	Sequence 2223, Ap
19	18	3.6	630	14	US-10-213-990-45	Sequence 45, Appl
20	14	2.8	505	17	US-10-877-849-42	Sequence 42, Appl
21	14	2.8	511	17	US-10-877-849-8	Sequence 8, Appl
22	14	2.8	609	17	US-10-877-849-38	Sequence 38, Appl
23	14	2.8	629	17	US-10-877-849-34	Sequence 34, Appl
24	14	2.8	640	17	US-10-877-007-22	Sequence 22, Appl
25	14	2.8	640	17	US-10-877-849-32	Sequence 32, Appl
26	14	2.8	640	17	US-10-877-849-41	Sequence 41, Appl
27	13	2.6	567	17	US-10-486-868-18	Sequence 18, Appl
28	12	2.4	500	15	US-10-369-493-12469	Sequence 12469, A
29	12	2.4	547	14	US-10-213-990-48	Sequence 48, Appl
30	12	2.4	549	17	US-10-486-868-14	Sequence 14, Appl
31	12	2.4	555	17	US-10-486-868-15	Sequence 15, Appl
32	11	2.2	484	15	US-10-416-393-1	Sequence 1, Appl
33	11	2.2	484	16	US-10-797-393A-1	Sequence 1, Appl
34	10	2.0	263	16	US-10-435-115-291647	Sequence 291647, A
35	9	1.8	90	16	US-10-437-963-169831	Sequence 169831, A
36	9	1.8	421	14	US-10-156-761-13129	Sequence 13129, A
37	9	1.8	561	15	US-10-369-493-12810	Sequence 12810, A
38	8	1.6	58	16	US-10-767-701-50236	Sequence 50236, A
39	8	1.6	84	15	US-10-424-599-284520	Sequence 284520, A
40	8	1.6	105	16	US-10-437-963-125916	Sequence 125916, A
41	8	1.6	134	16	US-10-437-963-129535	Sequence 129535, A
42	8	1.6	258	16	US-10-432-934-78	Sequence 78, Appl
43	8	1.6	400	15	US-10-282-122A-50565	Sequence 50565, A
44	8	1.6	454	16	US-10-437-963-143998	Sequence 143998, A
45	8	1.6	494	20	US-11-097-143-26370	Sequence 26370, A

ALIGNMENTS

RESULT 1
US-10-820-200-2
; Sequence 2, Application US/10820200
; Publication No. US20040229764A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Pedersen, Sven
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
; FILE REFERENCE: 5835.200-US
; CURRENT APPLICATION NUMBER: US/10/820,200
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US/09/710,339
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/165,786
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus Oryzae
US-10-820-200-2

Query Match	100.0%	Score 498;	DB 16;	Length 498;
Best Local Similarity	100.0%	Pred. No. 0;		
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Db	1	MVAWNSFLYGLQVAPALAAATPADWRQSISYFLLTDRFARTDGTATCNTADQKYCGG	60	
QY	61	TWQGLDKLDYICQGFATWITPTAQLPOTAGDAYHGYOODIVSLNENYGATDDL	120	

Db 61 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Qy 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHFPCFIONYEDQTQ 180
Db 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHFPCFIONYEDQTQ 180
Qy 181 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 240
Db 181 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 240
Qy 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNMINTVK 300
Db 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNMINTVK 300
Qy 301 SDPCPSTLLGTFFVENHNDNPRFASYNIDIALAKNVAAFIILNDGIPIIYAGQBOHYAGGND 360
Db 301 SDPCPSTLLGTFFVENHNDNPRFASYNIDIALAKNVAAFIILNDGIPIIYAGQBOHYAGGND 360
Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 420
Db 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 420
Qy 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
Db 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
Qy 481 RVLYPTEKLAGSKICSSS 498
Db 481 RVLYPTEKLAGSKICSSS 498

RESULT 2

US-10-877-849-30
; Sequence 30, Application US/10877849
; Publication No. US20050054071A1
; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Tkagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikeo-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-877-849-30

Query Match 100.0%; Score 498; DB 17; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGG 60
Db 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGG 60
Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Db 61 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Qy 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHFPCFIONYEDQTQ 180
Db 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHFPCFIONYEDQTQ 180
Qy 181 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 240
Db 181 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 240

Qy 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNMINTVK 300
Db 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNMINTVK 300
Qy 301 SDPCPSTLLGTFFVENHNDNPRFASYNIDIALAKNVAAFIILNDGIPIIYAGQBOHYAGGND 360
Db 301 SDPCPSTLLGTFFVENHNDNPRFASYNIDIALAKNVAAFIILNDGIPIIYAGQBOHYAGGND 360
Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 420
Db 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 420
Qy 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
Db 421 DGSQIVTILSNKGASGDSYTLISLGAGYTAGQQLTEVIGCTTIVTGVSDGNVPVPMAGGLP 480
Qy 481 RVLYPTEKLAGSKICSSS 498
Db 481 RVLYPTEKLAGSKICSSS 498

RESULT 3

US-10-797-393A-5
; Sequence 5, Application US/10797393A
; Publication No. US20040219649A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Hans Sejr
; APPLICANT: Pedersen, Sven
; APPLICANT: Festeren, Rikke Monica
; TITLE OF INVENTION: ALCOHOL PRODUCT PROCESSES
; FILE REFERENCE: 10391.200-US
; CURRENT APPLICATION NUMBER: US/10/797,393A
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-797-393A-5

Query Match 100.0%; Score 498; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGG 60
Db 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADQKCGG 61
Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVTALPQTAYGDAYHGYWQODIYSLNENYGTADDL 121
Qy 121 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHFPCFIONYEDQTQ 180
Db 122 KALSALHERGMYLMDVVANHMGVDGAGSSVDYSVFKPFSSQDYFHFPCFIONYEDQTQ 181
Qy 181 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 240
Db 182 VEDCWLGNVTSLPDLDTTKDVKWNEWYDWVGLSVNSYSDGLRDTTKVHKQKDFWPGYN 241
Qy 241 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNMINTVK 300
Db 242 KAAGYVCIGEVLDGDPAYTCYQNVMDGVLNPIIYPLLNAPKSTSGSMDDLYNMINTVK 301
Qy 301 SDPCPSTLLGTFFVENHNDNPRFASYNIDIALAKNVAAFIILNDGIPIIYAGQBOHYAGGND 360
Db 302 SDPCPSTLLGTFFVENHNDNPRFASYNIDIALAKNVAAFIILNDGIPIIYAGQBOHYAGGND 361
Qy 361 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 420
Db 362 PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKG 421


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; GENERAL INFORMATION:
; APPLICANT: Udagawa, Hiroaki
; APPLICANT: Taira, Rikako
; APPLICANT: Takagi, Shinobu
; APPLICANT: Allain, Eric
; APPLICANT: Hjort, Carsten
; APPLICANT: Vikeo-Nielsen, Anders
; TITLE OF INVENTION: HYBRID ENZYMES FOR STARCH PROCESSING
; FILE REFERENCE: 10490.500-US
; CURRENT APPLICATION NUMBER: US/10/877,849
; CURRENT FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 43
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
; NAME/KEY: mat_peptide
; LOCATION: (1)..(476)
US-10-877-849-43

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db      1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI 60

Qy      81 WITPVTALPQTAYGDAYHGYYWQDIYSLNENYGTADDLKSALSHALHERGMYLMDVVA 140
Db      61 WITPVTALPQTAYGDAYHGYYWQDIYSLNENYGTADDLKSALSHALHERGMYLMDVVA 120

Qy      141 NHMGYDAGSSVDYVFPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 200
Db      121 NHMGYDAGSSVDYVFPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 180

Qy      201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYKNAAGVYCI GEVL DGPAYTC 260
Db      181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYKNAAGVYCI GEVL DGPAYTC 240

Qy      261 PYQNVMDGVLYNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGTFFVENHNDNR 320
Db      241 PYQNVMDGVLYNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGTFFVENHNDNR 300

Qy      321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
Db      301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360

Qy      381 LIASANAIRNVAISKDTGFVTYKWPYKDDTIAMRKGTGDSQIVTILSKNGASGDSYT 440
Db      361 LIASANAIRNVAISKDTGFVTYKWPYKDDTIAMRKGTGDSQIVTILSKNGASGDSYT 420

Qy      441 LSLSGAGYTAGQQLTEVIGCTTGVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS 496
Db      421 LSLSGAGYTAGQQLTEVIGCTTGVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS 476

RESULT 7
US-10-184-771-10
; Sequence 10, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
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; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-10-184-771-10

Query Match      78.5%; Score 391; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db      1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNTADOKYCGGTWQGIIDKLDYIQGMGFTAI 60

Qy      81 WITPVTALPQTAYGDAYHGYYWQDIYSLNENYGTADDLKSALSHALHERGMYLMDVVA 140
Db      61 WITPVTALPQTAYGDAYHGYYWQDIYSLNENYGTADDLKSALSHALHERGMYLMDVVA 120

Qy      141 NHMGYDAGSSVDYVFPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 200
Db      121 NHMGYDAGSSVDYVFPFSSQDYFHPFCFQNYEDQTVEDCWLGDNVSLPDLDTTK 180

Qy      201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYKNAAGVYCI GEVL DGPAYTC 260
Db      181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYKNAAGVYCI GEVL DGPAYTC 240

Qy      261 PYQNVMDGVLYNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGTFFVENHNDNR 320
Db      241 PYQNVMDGVLYNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGTFFVENHNDNR 300

Qy      321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
Db      301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360

Qy      381 LIASANAIRNVAISKDTGFVTYKWPYKDD 411
Db      361 LIASANAIRNVAISKDTGFVTYKWPYKDD 391

RESULT 8
US-10-186-042-7
; Sequence 7, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
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US-10-186-042-7

Query Match 78.5%; Score 391; DB 14; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSOSIYFLLTDRPARTDGSSTATCNTADQKCCGWTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSOSIYFLLTDRPARTDGSSTATCNTADQKCCGWTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTALPQTAYGDAYHYGQQDIYSLNENYGTADDLKALSSALHERGMVLMVDVVA 140
DB 61 WITPVTALPQTAYGDAYHYGQQDIYSLNENYGTADDLKALSSALHERGMVLMVDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYPHPFCFQNYEDQTVQVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFKPFSSQDYPHPFCFQNYEDQTVQVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNNMINTVKS DCPDSTLLGTFFVENHDNPR 320
DB 241 PYQNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNNMINTVKS DCPDSTLLGTFFVENHDNPR 300
QY 321 FASYTNDIALAKNVAFIILNDGIPIIYAGQHQHAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAFIILNDGIPIIYAGQHQHAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNYAISKDTGFVTKNWPYKDD 411
DB 361 LIASANAIRNYAISKDTGFVTKNWPYKDD 391

RESULT 9

US-10-644-187-7
; Sequence 7, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-644-187-7

Query Match 78.5%; Score 391; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSOSIYFLLTDRPARTDGSSTATCNTADQKCCGWTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSOSIYFLLTDRPARTDGSSTATCNTADQKCCGWTWQGIIDKLDYIQGMGFTAI 60

QY 81 WITPVTALPQTAYGDAYHYGQQDIYSLNENYGTADDLKALSSALHERGMVLMVDVVA 140
DB 61 WITPVTALPQTAYGDAYHYGQQDIYSLNENYGTADDLKALSSALHERGMVLMVDVVA 120
QY 141 NHMGYDAGSSVDYSVFKPFSSQDYPHPFCFQNYEDQTVQVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFKPFSSQDYPHPFCFQNYEDQTVQVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
DB 181 DVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
QY 261 PYQNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNNMINTVKS DCPDSTLLGTFFVENHDNPR 320
DB 241 PYQNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNNMINTVKS DCPDSTLLGTFFVENHDNPR 300
QY 321 FASYTNDIALAKNVAFIILNDGIPIIYAGQHQHAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAFIILNDGIPIIYAGQHQHAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNYAISKDTGFVTKNWPYKDD 411
DB 361 LIASANAIRNYAISKDTGFVTKNWPYKDD 391

RESULT 10

US-10-926-720-10
; Sequence 10, Application US/10926720
; Publication No. US20050019886A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/926,720
; FILING DATE: 26-AUG-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-926-720-10

Query Match 78.5%; Score 391; DB 17; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQMGFTAI 80
|||||
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQMGFTAI 60
|||||

QY 81 WITPVTAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
|||||
Db 61 WITPVTAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
|||||

QY 141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 200
|||||
Db 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 180
|||||

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVL DGD PAYTC 260
|||||
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVL DGD PAYTC 240
|||||

QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGT FVENH DNPR 320
|||||
Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGT FVENH DNPR 300
|||||

QY 321 FASYTNDIALAKNVAAFIILNDGPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
|||||
Db 301 FASYTNDIALAKNVAAFIILNDGPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360
|||||

QY 381 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 411
|||||
Db 361 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 391
|||||

RESULT 11

US-10-980-759-7
; Sequence 7, Application US/10980759
; Publication No. US20050118695A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796-204-US
; CURRENT APPLICATION NUMBER: US/10/980,759
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis

Query Match 78.5%; Score 391; DB 17; Length 478;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQMGFTAI 80
|||||
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQMGFTAI 60
|||||

QY 81 WITPVTAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
|||||

Db 61 WITPVTAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
|||||

QY 141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 200
|||||

Db 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 180
|||||

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVL DGD PAYTC 260
|||||

Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVL DGD PAYTC 240
|||||

QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGT FVENH DNPR 320
|||||

Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGT FVENH DNPR 300
|||||

QY 321 FASYTNDIALAKNVAAFIILNDGPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
|||||

Db 301 FASYTNDIALAKNVAAFIILNDGPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 360
|||||

QY 381 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 411
|||||

Db 361 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 391
|||||

RESULT 12
US-11-064-196-10
; Sequence 10, Application US/11064196
; Publication No. US20050170487A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1P216-US2
; CURRENT APPLICATION NUMBER: US/11/064,196
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae

Query Match 78.5%; Score 391; DB 20; Length 478;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQMGFTAI 80
|||||

Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTTATCNADOKYCGGTWQGIIDKLDYIQMGFTAI 60
|||||

QY 81 WITPVTAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
|||||

Db 61 WITPVTAQLPQTAYGDAYHGHWQODIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
|||||

QY 141 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 200
|||||

Db 121 NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGNTVSLPDLDTTK 180
|||||

QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVL DGD PAYTC 260
|||||

Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYCI GEVL DGD PAYTC 240
|||||

QY 261 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGT FVENH DNPR 320
|||||

Db 241 PYQNVMDGVLNPIYIYPLLNAPKSTSGSMDDLNNMINTVKS DCPDSTLLGT FVENH DNPR 300
|||||

QY 321 FASYTNDIALAKNVAAFIILNDGPIIYAGQOHYAGGNDPANREATWLSGYPTDSELYK 380
|||||

Db 301 FASYTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGNDPANREATWLSGYPTDSELYK 360
Qy 381 LIASANAIRNYAISKDTGFVYKNWPIYKDD 411
Db 361 LIASANAIRNYAISKDTGFVYKNWPIYKDD 391

RESULT 13

US-10-815-495-22
; Sequence 22, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connolly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495
; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-22

Query Match 77.1%; Score 384; DB 16; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVAWNSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 60
Db 2 MVAWNSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 61

Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL 121

Qy 121 KALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQQT 180
Db 122 KALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQQT 181

Qy 181 VEDCWLGDNVSLPDLDTTKDVVKNEWYDWVGSLSVNSYSDGLRIDTVKHVQKDFWPGYN 240
Db 182 VEDCWLGDNVSLPDLDTTKDVVKNEWYDWVGSLSVNSYSDGLRIDTVKHVQKDFWPGYN 241

Qy 241 KAAGVYCIGEVLDGDPAYTCYQNVMDGVNLNPIYPLNNAFKSTSGSMDLLNMINTVK 300
Db 242 KAAGVYCIGEVLDGDPAYTCYQNVMDGVNLNPIYPLNNAFKSTSGSMDLLNMINTVK 301

Qy 301 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGND 360
Db 302 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGND 361

Qy 361 PANREATWLSGYPTDSELYKLIAS 384
Db 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 14

US-10-815-495-18
; Sequence 18, Application US/10815495
; Publication No. US20040191864A1
; GENERAL INFORMATION:
; APPLICANT: Novozymes Biotech, Inc.
; APPLICANT: Connolly, Mariah
; APPLICANT: Brody, Howard
; TITLE OF INVENTION: Methods For Producing Biological Substances In Enzyme-Deficient
; TITLE OF INVENTION: Mutants Of Aspergillus Niger
; FILE REFERENCE: 10345.200-US
; CURRENT APPLICATION NUMBER: US/10/815,495

; CURRENT FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-815-495-18

Query Match 77.1%; Score 384; DB 16; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVAWNSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 60
Db 2 MVAWNSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGG 61

Qy 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL 120
Db 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL 121

Qy 121 KALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQQT 180
Db 122 KALSSALHERGMVLMVDVNVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQQT 181

Qy 181 VEDCWLGDNVSLPDLDTTKDVVKNEWYDWVGSLSVNSYSDGLRIDTVKHVQKDFWPGYN 240
Db 182 VEDCWLGDNVSLPDLDTTKDVVKNEWYDWVGSLSVNSYSDGLRIDTVKHVQKDFWPGYN 241

Qy 241 KAAGVYCIGEVLDGDPAYTCYQNVMDGVNLNPIYPLNNAFKSTSGSMDLLNMINTVK 300
Db 242 KAAGVYCIGEVLDGDPAYTCYQNVMDGVNLNPIYPLNNAFKSTSGSMDLLNMINTVK 301

Qy 301 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGND 360
Db 302 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEQHYAGGND 361

Qy 361 PANREATWLSGYPTDSELYKLIAS 384
Db 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 15

US-10-228-063-45
; Sequence 45, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Aspergillus shiroleusami
US-10-228-063-45

Query Match 75.7%; Score 377; DB 14; Length 1095;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60

Qy 81 WITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL KALSSALHERGMVLMVDVVA 140
Db 61 WITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL KALSSALHERGMVLMVDVVA 120

Qy 141 NEMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQQTQVEDCWLGDNVSLPDLDTTK 200

Db	121	NHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTK	180
Qy	201	DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGYVCIGEVLDGDPAYTC	260
Db	181	DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGYVCIGEVLDVDPAYTC	240
Qy	261	PYQNVMGVLNYPYIYPLNNAFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDNR	320
Db	241	PYQNVMGVLNYPYIYPLNNAFKSTSGSMDDLNNMINTVKSDCPDSTLLGTFFVENHNDNR	300
Qy	321	FASYTNDIALAKNVAAFIILNDGIPIIYAGQHQHYAGGNDPANREATWLSGYPTDSELYK	380
Db	301	FASYTNDIALAKNVAAFIILNDGIPIIYAGQHQHYAGGNDPANREATWLSGYPTDSELYK	360
Qy	381	LIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT	440
Db	361	LIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKGTGDSQIVTILSNKGASGDSYT	420
Qy	441	LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS	498
Db	421	LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKICSSS	478

Search completed: November 7, 2005, 19:22:49
Job time : 267.305 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:45:18 ; Search time 74.9884 Seconds
(without alignments)
495.746 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
Sequence: 1 MVAMWSFLYGLQVAAPALA.....LPRVLYPTEKLAGSKICSSS 498

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	391	78.5	478	1	US-08-720-899-7
2	391	78.5	478	1	US-08-459-610-7
3	391	78.5	478	2	US-08-343-804-7
4	391	78.5	478	2	US-08-600-908A-10
5	391	78.5	478	3	US-08-683-838A-10
6	391	78.5	478	3	US-09-182-859-7
7	391	78.5	478	4	US-09-672-459-7
8	391	78.5	478	4	US-09-636-252A-10
9	391	78.5	478	4	US-10-186-042-7
10	238	47.8	478	2	US-08-339-715A-2
11	18	3.6	304	3	US-09-189-060B-72
12	18	3.6	304	3	US-09-189-060B-66
13	18	3.6	306	3	US-09-189-060B-68
14	18	3.6	307	3	US-09-189-060B-74
15	18	3.6	308	3	US-09-189-060B-70
16	11	2.2	468	1	US-08-204-656B-2
17	11	2.2	468	1	US-08-204-656B-4
18	11	2.2	468	1	US-08-204-656B-6
19	11	2.2	468	1	US-08-204-656B-8
20	11	2.2	468	1	US-08-470-702-6
21	11	2.2	468	1	US-08-470-702-7
22	11	2.2	468	1	US-08-470-702-8
23	11	2.2	468	1	US-08-470-702-9
24	11	2.2	468	1	US-08-467-831-6
25	11	2.2	468	1	US-08-467-831-7
26	11	2.2	468	1	US-08-467-831-8
27	11	2.2	468	1	US-08-467-831-9

28	8	1.6	450	4	US-09-252-991A-25354	Sequence 25354, A
29	8	1.6	477	4	US-09-134-000C-4388	Sequence 4388, Ap
30	8	1.6	2039	4	US-09-077-098A-7	Sequence 7, Appli
31	7	1.4	22	3	US-09-613-182-7	Sequence 7, Appli
32	7	1.4	63	4	US-09-248-796A-25725	Sequence 25725, A
33	7	1.4	63	4	US-09-513-998C-4374	Sequence 4374, A
34	7	1.4	117	4	US-09-647-468-142	Sequence 142, App
35	7	1.4	119	4	US-09-647-468-30	Sequence 30, Appl
36	7	1.4	119	4	US-09-647-468-40	Sequence 40, Appl
37	7	1.4	119	4	US-09-647-468-42	Sequence 42, Appl
38	7	1.4	119	4	US-09-647-468-50	Sequence 50, Appl
39	7	1.4	119	4	US-09-647-468-52	Sequence 52, Appl
40	7	1.4	119	4	US-09-647-468-58	Sequence 58, Appl
41	7	1.4	119	4	US-09-647-468-60	Sequence 60, Appl
42	7	1.4	119	4	US-09-647-468-64	Sequence 64, Appl
43	7	1.4	119	4	US-09-647-468-70	Sequence 70, Appl
44	7	1.4	119	4	US-09-647-468-72	Sequence 72, Appl
45	7	1.4	119	4	US-09-647-468-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1

US-08-720-899-7
; Sequence 7, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: NO. 57534600 No. 5753460disk of No. 5753460ch America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-720-899-7

Query Match 78.5%; Score 391; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	21	ATPADWRSOSIYFLLTD	FARTDGS	TTCNTADQK	CGGTWQGI	IDKLYI	IQMGFTAI	80
Db	1	ATPADWRSOSIYFLLTD	FARTDGS	TTCNTADQK	CGGTWQGI	IDKLYI	IQMGFTAI	60
Qy	81	WITPVTAQLPQTATY	GDAYHGWQODIY	SLNENGTADDL	KALSSALHERGMYL	WDDVVA	140	
Db	61	WITPVTAQLPQTATY	GDAYHGWQODIY	SLNENGTADDL	KALSSALHERGMYL	WDDVVA	120	
Qy	141	NHMGYDGAGSSVDY	SFVKPFSSQDY	FHFPCFIQNYE	QTOVEDCWLGDNTV	SLPDLDTTK	200	
Db	121	NHMGYDGAGSSVDY	SFVKPFSSQDY	FHFPCFIQNYE	QTOVEDCWLGDNTV	SLPDLDTTK	180	
Qy	201	DVYKNEWYDWGSL	SNYSISIDGLRIDT	VKHVKQDFWFGY	NKAAGVYICGBVL	DGDDPAYTC	260	
Db	181	DVYKNEWYDWGSL	SNYSISIDGLRIDT	VKHVKQDFWFGY	NKAAGVYICGBVL	DGDDPAYTC	240	
Qy	261	PYQVNVMDGVLNPIY	YIYPLLNAFKSTG	SMDDLYNNMINTV	KSDCPDSTLLGTF	FVENHDNPR	320	
Db	241	PYQVNVMDGVLNPIY	YIYPLLNAFKSTG	SMDDLYNNMINTV	KSDCPDSTLLGTF	FVENHDNPR	300	
Qy	321	FASYTNDIALAKN	VAAFIILNDGPIIY	IYAGOEQHYAGGN	DPANREATWLSGY	PTDSELYK	380	
Db	301	FASYTNDIALAKN	VAAFIILNDGPIIY	IYAGOEQHYAGGN	DPANREATWLSGY	PTDSELYK	360	
Qy	381	LIASANAIRNYAI	SKDTGFVYK	NWPIYKDD	411			
Db	361	LIASANAIRNYAI	SKDTGFVYK	NWPIYKDD	391			

RESULT 2

US-08-459-610-7
: Sequence 7, Application US/08459610
: Patent No. 5801043
: GENERAL INFORMATION:
: APPLICANT: Bisgaard-Frantzen, Henrik
: APPLICANT: Borchert, Torben Vedel
: APPLICANT: Svendsen, Allan
: APPLICANT: Thellersen, Marianne
: APPLICANT: Van der Zee, Pia
: TITLE OF INVENTION: AMYLASE VARIANTS
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
: STREET: 405 Lexington Avenue, 64th Floor
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,610
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/343,804
: FILING DATE: 22-NOV-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lowney Dr., Karen A.
: REGISTRATION NUMBER: 31,274
: REFERENCE/DOCKET NUMBER: 4054,214-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-867-0123
: TELEFAX: 212-878-9655
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 478 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear

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US-08-459-610-7
Query Match          78.5%; Score 391; DB 1; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTATTCTNADQKYCGGTWQGIIDKLDYIQMGFTAI 60

Qy 81 WITPVTVAQLPQTAYGDAYGHGYWQDIYSLNENYGTADDLKALSSALHERGMYLWVDVVA 140
Db 61 WITPVTVAQLPQTAYGDAYGHGYWQDIYSLNENYGTADDLKALSSALHERGMYLWVDVVA 120

Qy 141 NHMGYDGAGSSVDYSVFKPSSQDYFHPFCFIQNYEDQTOVEDCWLGDNTVSLPDLDTTK 200
Db 121 NHMGYDGAGSSVDYSVFKPSSQDYFHPFCFIQNYEDQTOVEDCWLGDNTVSLPDLDTTK 180

Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDIVKHVQKDFWFGYNKAAGVYCIGEVLDDGPAVTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDIVKHVQKDFWFGYNKAAGVYCIGEVLDDGPAVTC 240

Qy 261 PYQNVMDGVLNPIIYPLLNAFSTSGSMDLLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
Db 241 PYQNVMDGVLNPIIYPLLNAFSTSGSMDLLYNMINTVKSDCPDSTLLGTFVENHDNPR 300

Qy 321 FASYTNDIALAKNVAAPFIILNDGPIIYAGOEQHYAGNDPANREATWLSGYPTDSELYK 380
Db 301 FASYTNDIALAKNVAAPFIILNDGPIIYAGOEQHYAGNDPANREATWLSGYPTDSELYK 360

Qy 381 LIASANAIRNYAISKDTGFVYKNWPIYKDD 411
Db 361 LIASANAIRNYAISKDTGFVYKNWPIYKDD 391

RESULT 3
US-08-343-804-7
; Sequence 7, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thøllersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids

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;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-343-804-7

Query Match 78.5%; Score 391; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ATPADWRSOSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSOSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
Qy 81 WITPVTQAQLPQTAYGDAYHYGYWQDIYSLNENYGTADDLKALSSALHHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHYGYWQDIYSLNENYGTADDLKALSSALHHERGMYLMDVVA 120
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Db 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVQVDCWLGDNVSLPDLDTTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCIGEVLDGDPAYTC 240
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Db 241 PQYNVMDGVLNPIYYPYLLNAPFKSTSGSMDLLYNMINTVKSDCPDSTLLGTFFVENHDNPR 300
Qy 321 FASYTNDIALAKNVAAFIINDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSSELYK 380
Db 301 FASYTNDIALAKNVAAFIINDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSSELYK 360
Qy 381 LIASANAIRNAYAIKSDTGFVYKNWPIYKDD 411
Db 361 LIASANAIRNAYAIKSDTGFVYKNWPIYKDD 391

RESULT 4
US-08-600-908A-10
; Sequence 10, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169 No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-600-908A-10

Query Match 78.5%; Score 391; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ATPADWRSOSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSOSIYFLLTDRFARTDGTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAI 60
Qy 81 WITPVTQAQLPQTAYGDAYHYGYWQDIYSLNENYGTADDLKALSSALHHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHYGYWQDIYSLNENYGTADDLKALSSALHHERGMYLMDVVA 120
Qy 141 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVQVDCWLGDNVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYVFKPFSSQDYFHPFCFIQNYEDQTVQVDCWLGDNVSLPDLDTTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAAGVYCIGEVLDGDPAYTC 240
Qy 261 PQYNVMDGVLNPIYYPYLLNAPFKSTSGSMDLLYNMINTVKSDCPDSTLLGTFFVENHDNPR 320
Db 241 PQYNVMDGVLNPIYYPYLLNAPFKSTSGSMDLLYNMINTVKSDCPDSTLLGTFFVENHDNPR 300
Qy 321 FASYTNDIALAKNVAAFIINDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSSELYK 380
Db 301 FASYTNDIALAKNVAAFIINDGIPIIYAGQEOHYAGGNDPANREATWLSGYPTDSSELYK 360
Qy 381 LIASANAIRNAYAIKSDTGFVYKNWPIYKDD 411
Db 361 LIASANAIRNAYAIKSDTGFVYKNWPIYKDD 391

RESULT 5
US-08-683-838A-10
; Sequence 10, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6022724 No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-683-838A-10

Query Match 78.5%; Score 391; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGYYWQDIYSLNENYGTADDLKALSSALHERGMYLWVDVVA 140
DB 61 WITPVTAQLPQTAYGDAYHGYYWQDIYSLNENYGTADDLKALSSALHERGMYLWVDVVA 120
QY 141 NHMGYDAGSSVDYSVFEPFSSQDYFHPFCFIONYEDQTVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFEPFSSQDYFHPFCFIONYEDQTVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICGEVLDDGDPAYTC 260
DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICGEVLDDGDPAYTC 240
QY 261 PYQNVMDGVLNYPPIYYPLLNAPKSTSGMDDLNNINTVKSDCPDSTLLGTTFVENHNDNR 320
DB 241 PYQNVMDGVLNYPPIYYPLLNAPKSTSGMDDLNNINTVKSDCPDSTLLGTTFVENHNDNR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTYKKNWPIYKDD 411
DB 361 LIASANAIRNVAISKDTGFTYKKNWPIYKDD 391

RESULT 6

US-09-182-859-7
; Sequence 7, Application US/09182859
; Patent No. 6143708
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/182,859
; CURRENT FILING DATE: 1998-10-29
; EARLIER APPLICATION NUMBER: 0515/96
; EARLIER FILING DATE: 1996-04-30
; EARLIER APPLICATION NUMBER: 0712/96
; EARLIER FILING DATE: 1996-06-28
; EARLIER APPLICATION NUMBER: 0775/96
; EARLIER FILING DATE: 1996-07-11
; EARLIER APPLICATION NUMBER: 1263/96
; EARLIER FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-182-859-7

Query Match 78.5%; Score 391; DB 3; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGYYWQDIYSLNENYGTADDLKALSSALHERGMYLWVDVVA 140
DB 61 WITPVTAQLPQTAYGDAYHGYYWQDIYSLNENYGTADDLKALSSALHERGMYLWVDVVA 120
QY 141 NHMGYDAGSSVDYSVFEPFSSQDYFHPFCFIONYEDQTVEDCWLGDNTVSLPDLDTTK 200
DB 121 NHMGYDAGSSVDYSVFEPFSSQDYFHPFCFIONYEDQTVEDCWLGDNTVSLPDLDTTK 180
QY 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICGEVLDDGDPAYTC 260
DB 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGVYICGEVLDDGDPAYTC 240
QY 261 PYQNVMDGVLNYPPIYYPLLNAPKSTSGMDDLNNINTVKSDCPDSTLLGTTFVENHNDNR 320
DB 241 PYQNVMDGVLNYPPIYYPLLNAPKSTSGMDDLNNINTVKSDCPDSTLLGTTFVENHNDNR 300
QY 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 380
DB 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQEHYAGGNDPANREATWLSGYPTDSELYK 360
QY 381 LIASANAIRNVAISKDTGFTYKKNWPIYKDD 411
DB 361 LIASANAIRNVAISKDTGFTYKKNWPIYKDD 391

RESULT 7

US-09-672-459-7
; Sequence 7, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672,459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-7

Query Match 78.5%; Score 391; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
DB 1 ATPADWRSQSIYFLLTDRPARTDGSSTTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
QY 81 WITPVTAQLPQTAYGDAYHGYYWQDIYSLNENYGTADDLKALSSALHERGMYLWVDVVA 140

Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
Qy 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
Qy 261 PQYNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNMINTVKSDDPSTLLGTFFVENHDNPR 320
Db 241 PQYNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNMINTVKSDDPSTLLGTFFVENHDNPR 300
Qy 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 360
Qy 381 LIASANAIRNVAISKDTGFVTKNMPYKDD 411
Db 361 LIASANAIRNVAISKDTGFVTKNMPYKDD 391

RESULT 8

US-09-636-252A-10
; Sequence 10, Application US/09636252A
; Patent No. 6440716
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1P216-US2
; CURRENT APPLICATION NUMBER: US/09/636,252A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 478
; TYPE: PRT
; ORGANISM: A. oryzae
US-09-636-252A-10

Query Match 78.5%; Score 391; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ATPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
Qy 81 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
Qy 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
Qy 261 PQYNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNMINTVKSDDPSTLLGTFFVENHDNPR 320
Db 241 PQYNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNMINTVKSDDPSTLLGTFFVENHDNPR 300
Qy 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 360

Qy 381 LIASANAIRNVAISKDTGFVTKNMPYKDD 411
Db 361 LIASANAIRNVAISKDTGFVTKNMPYKDD 391

RESULT 9

US-10-186-042-7
; Sequence 7, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186,042
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-7

Query Match 78.5%; Score 391; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ATPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 80
Db 1 ATPADWRSQSIYFLLTDRFARTDGSSTATCNTADQKCGGTWQGIIDKLDYIQGMGFTAI 60
Qy 81 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
Db 61 WITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
Qy 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
Db 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
Qy 201 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 260
Db 181 DVVKNEWYDWGSLVSNYSIDGLRIDTVKHQKDFWPGYNKAAGVYICIGEVLDGDPAYTC 240
Qy 261 PQYNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNMINTVKSDDPSTLLGTFFVENHDNPR 320
Db 241 PQYNVMDGVLNPIIYYPPLNAFKSTSGSMDLLYNMINTVKSDDPSTLLGTFFVENHDNPR 300
Qy 321 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 380
Db 301 FASYTNDIALAKNVAAFIILNDGIPIIYAGQOHYAGGNDPANREATWLSGYPTDSLYK 360
Qy 381 LIASANAIRNVAISKDTGFVTKNMPYKDD 411
Db 361 LIASANAIRNVAISKDTGFVTKNMPYKDD 391

RESULT 10

US-08-339-715A-2
; Sequence 2, Application US/08339715A

; Patent No. 5965442
; GENERAL INFORMATION:
; APPLICANT: Kaneko, Hiroki
; APPLICANT: Takada, Toshikazu
; APPLICANT: Shimada, Jiro
; APPLICANT: Kuriki, Takashi
; APPLICANT: Yanase, Michio
; APPLICANT: Takata, Hiroki
; APPLICANT: Okada, Shigetaka
; TITLE OF INVENTION: METHOD OF ALTERING ENZYMES AND A NOVEL
; TITLE OF INVENTION: NEOPULLULANASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: POHAM, HAIK, SCHNOBICH & KAUFMAN, LTD.
; STREET: Metropolitan Square Building, Suite 800, 1450
; STREET: G. Street
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,715A
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306096/1993
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Welser, Allen S.
; REGISTRATION NUMBER: 27,215
; REFERENCE/DOCKET NUMBER: 18335.009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-824-8000
; TELEFAX: 202-824-8199
; TELEX: 248516
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-715A-2

Query Match 47.8%; Score 238; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.1e-219; Mismatches 0; Indels 0; Gaps 0;
Matches 238; Conservative 0;
QY 106 DIYSLNENYGTDADLKALSSALHGERGYLMVDVNVANHMGYDAGSSVDYSVFKPSSQDY 165
Db |||||
86 DIYSLNENYGTDADLKALSSALHGERGYLMVDVNVANHMGYDAGSSVDYSVFKPSSQDY 145
QY 166 FHPFCFIQNYEDQTOVEDCWLGDNVTSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRI 225
Db |||||
146 FHPFCFIQNYEDQTOVEDCWLGDNVTSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRI 205
QY 226 DTVKHVQKDFWPGYNKAAGVYICIGVLGDPAITCPYQNVMDGVNLNPIYYPLLNAPKST 285
Db |||||
206 DTVKHVQKDFWPGYNKAAGVYICIGVLGDPAITCPYQNVMDGVNLNPIYYPLLNAPKST 265
QY 286 SGSMDDLNNMINTVKSCDPCDSTLLGTFFVENHDNPRFASVYNDIALAKNVAAPFIILNDG 343
Db |||||
266 SGSMDDLNNMINTVKSCDPCDSTLLGTFFVENHDNPRFASVYNDIALAKNVAAPFIILNDG 323

RESULT 11
US-09-189-060B-72
; Sequence 72, Application US/09189060B

; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Hybrid
; US-09-189-060B-72

Query Match 3.6%; Score 18; DB 3; Length 304;
Best Local Similarity 100.0%; Pred. No. 6.2e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 MVAWWSFLYGLQVAAPA 18
Db |||||
2 MVAWWSFLYGLQVAAPA 19

RESULT 12
US-09-189-060B-66
; Sequence 66, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B
; CURRENT FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/DK97/00216
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Hybrid
; US-09-189-060B-66

Query Match 3.6%; Score 18; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 6.2e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 MVAWWSFLYGLQVAAPA 18
Db |||||
4 MVAWWSFLYGLQVAAPA 21

RESULT 13
US-09-189-060B-68
; Sequence 68, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Markus
; APPLICANT: Borge, Diderichsen
; TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
; FILE REFERENCE: 4772.204-US
; CURRENT APPLICATION NUMBER: US/09/189,060B

Query Match 3.6%; Score 18; DB 3; Length 306;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAWMSFLYGLQVAAPA 18
DB 4 MVAWMSFLYGLQVAAPA 21

Query Match 3.6%; Score 18; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWMSFLYGLQVAAPA 18
DB 4 MVAWMSFLYGLQVAAPA 21

Query Match 3.6%; Score 18; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAWMSFLYGLQVAAPA 18
DB 4 MVAWMSFLYGLQVAAPA 21

Query Match 3.6%; Score 18; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWMSFLYGLQVAAPA 18
DB 4 MVAWMSFLYGLQVAAPA 21

Query Match 3.6%; Score 18; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAWMSFLYGLQVAAPA 18
DB 4 MVAWMSFLYGLQVAAPA 21

Query Match 3.6%; Score 18; DB 3; Length 308;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAWMSFLYGLQVAAPA 18
DB 4 MVAWMSFLYGLQVAAPA 21

Search completed: November 7, 2005, 19:00:08
Job time : 75.9884 secs

1900-1901 (1900-1901)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:15:40 ; Search time 60.5676 Seconds
(without alignments)
791.116 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
Sequence: 1 MWAWSLFLYGLQVAAPALA.....LPRVLYPTKLAGSKICSSS 498

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	499	1 ALAS1	alpha-amylase (EC
2	397	79.7	499	2 JS0663	alpha-amylase (EC
3	384	77.1	498	2 A48305	alpha-amylase (EC
4	384	77.1	499	2 B48305	alpha-amylase (EC
5	342	68.7	499	1 ALAS3	alpha-amylase (EC
6	296	59.4	499	2 JN0588	alpha-amylase (EC
7	244	49.0	499	2 JT0466	alpha-amylase (EC
8	238	47.8	478	2 JK0201	alpha-amylase (EC
9	20	4.0	507	2 S33921	alpha-amylase (EC
10	19	3.8	512	2 S23355	alpha-amylase (EC
11	19	3.8	512	2 S06115	alpha-amylase (EC
12	19	3.8	513	2 T38770	alpha-amylase a pr
13	16	3.2	624	1 JC4510	pullulanase (EC 3.
14	14	2.8	484	1 A35282	alpha-amylase (EC
15	12	2.4	482	2 S31478	alpha-amylase (EC
16	12	2.4	1196	2 A29130	beta-amylase (EC 3
17	11	2.2	494	1 ALBYAF	alpha-amylase (EC
18	10	2.0	625	2 T41603	alpha-amylase - fi
19	10	2.0	631	2 S72270	alpha-amylase (EC
20	9	1.8	581	2 S62505	probable alpha-am
21	8	1.6	140	2 H75368	hypothetical prote
22	8	1.6	149	2 G87329	hypothetical prote
23	8	1.6	151	2 A86695	hypothetical prote
24	8	1.6	160	2 E72529	hypothetical prote
25	8	1.6	258	2 C70968	probable ribD - My
26	8	1.6	305	2 H83344	hypothetical prote
27	8	1.6	326	2 C82200	cytochrome c oxida
28	8	1.6	494	1 A25529	alpha-amylase (EC
29	8	1.6	494	2 S58964	alpha-amylase (EC

30	8	1.6	494	2 S58960	alpha-amylase (EC
31	8	1.6	494	2 S58962	alpha-amylase (EC
32	8	1.6	494	2 S58953	alpha-amylase (EC
33	8	1.6	494	2 S58956	alpha-amylase (EC
34	8	1.6	494	2 S58958	alpha-amylase (EC
35	8	1.6	494	2 S58957	alpha-amylase (EC
36	8	1.6	494	2 S58965	alpha-amylase (EC
37	8	1.6	494	2 S58951	alpha-amylase (EC
38	8	1.6	494	2 S58954	alpha-amylase (EC
39	8	1.6	494	2 A60766	alpha-amylase (EC
40	8	1.6	623	2 T35377	probable membrane
41	8	1.6	690	2 B82409	alpha-amylase VCA0
42	8	1.6	774	2 T39539	alpha-amylase homo
43	8	1.6	829	2 E87305	TonB-dependent rec
44	8	1.6	919	2 S28179	alpha-amylase (EC
45	8	1.6	1036	2 AG1326	alpha-mannosidase

ALIGNMENTS

RESULT 1

ALAS1

alpha-amylase (EC 3.2.1.1) 1 precursor [validated] - Aspergillus oryzae
N:Alternate names: alpha-amylase isozyme II; glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C:Accession: S04548; A33214; JS0240; A91930; A93767; A10627
R:Wirsal, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A:Title: Three alpha-amylase genes of aspergillus oryzae exhibit identical intron-exon
A:Reference number: S04548; MUID:89237897; PMID:2785629
A:Accession: S04548
A:Molecule type: DNA
A:Residues: 1-499 <WIR>
A:Cross-references: UNIPROT:P10529; EMBL:X12725; NID:G2430; PIDN:CAA31218.1; PID:G29592
A:Genetics: AMY1
A:Accession: A33214
A:Molecule type: mRNA
A:Residues: 1-499 <W12>
A:Cross-references: GB:X12725; NID:G2430; PIDN:CAA31218.1; PID:G295921
R:Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989

A:Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin
A:Reference number: JS0240; MUID:89378767; PMID:2789162
A:Accession: JS0240
A:Molecule type: DNA
A:Residues: 1-499 <GEN>
A:Genetics: AMY2
A>Note: the authors refer to this as isozyme II
R:Isemura, S.; Ikenaka, T.
J. Biochem. 74, 1-10, 1973
A:Reference number: A91930; MUID:74001521; PMID:4733850
A:Accession: A91930
A:Molecule type: protein
A:Residues: 206-225 <ISE>
R:Narita, K.
Proc. Jpn. Acad. 51, 285-290, 1975
A:Reference number: A93767
A:Accession: A93767
A:Molecule type: protein
A:Residues: 434-443,446-447, 'Q',449-458, 'G'NTV, '459-464,467-468, 'B',470, 'B',472-499 <NAR
R:Matsumura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A:Title: Structure and possible catalytic residues of Taka-amylase A.
A:Reference number: A37454; MUID:84212370; PMID:6609921
A:Contents: annotation; X-ray crystallography, 3.0 angstroms
R:Swift, H.J.; Brady, L.; Derewenda, Z.S.; Dodson, E.J.; Turkmenburg, J.P.; Wilkinson, A
submitted to the Brookhaven Protein Data Bank, August 1992
A:Reference number: A51548; PDB:6TAA
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 22-497
C:Comment: One atom of calcium per molecule is essential for activity.
C:Genetics: <AMY1>

A;Gene: amy1
A;Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Genetics: <AMY2>
A;Gene: amy2; AmyII
A;Introns: 56/3; 65/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; polysaccharide
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase core homology <AMY>
F;51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F;142,183,196,231/Binding site: calcium (Asn, Glu, His) #status predicted
F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;227,251,318/Active site: Asp, Glu, Asp #status predicted

Query Match	100.0%;	Score 498;	DB 1;	Length 499;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 498;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	MVAVNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGG	60		
Db 2	MVAVNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGG	61		
Qy 61	TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL	120		
Db 62	TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL	121		
Qy 121	KALSSALHERGMYLMDVVDVVAHMGYDGGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ	180		
Db 122	KALSSALHERGMYLMDVVDVVAHMGYDGGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ	181		
Qy 181	VEDCWLGNTVSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPFGYN	240		
Db 182	VEDCWLGNTVSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPFGYN	241		
Qy 241	KAAGVYCIGEVLDGDPATCTPQNVMDGVLNPIYIYPLLNAPKSTGSMDDLNNMINTVK	300		
Db 242	KAAGVYCIGEVLDGDPATCTPQNVMDGVLNPIYIYPLLNAPKSTGSMDDLNNMINTVK	301		
Qy 301	SDCPDSTLLGTFFVENHNDPRFASVTNDIALAKNVAFAFIILNDGIPILYAGQEQHYAGGND	360		
Db 302	SDCPDSTLLGTFFVENHNDPRFASVTNDIALAKNVAFAFIILNDGIPILYAGQEQHYAGGND	361		
Qy 361	PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKKNWPIYKDDTTIAMRKGT	420		
Db 362	PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKKNWPIYKDDTTIAMRKGT	421		
Qy 421	DGSOQVITILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTGTGSDGNVPVPMAGGLP	480		
Db 422	DGSOQVITILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTGTGSDGNVPVPMAGGLP	481		
Qy 481	RVLYPTEKLAGSKICSSS 498			
Db 482	RVLYPTEKLAGSKICSSS 499			

RESULT 2
JS0663
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus sp.
C;Species: Aspergillus sp.
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 17-Mar-1999
C;Accession: JS0663
R;Shibuya, I.; Tamura, G.; Ishikawa, T.; Hara, S.
Biosci. Biotechnol. Biochem. 56, 174-179, 1992
A;Title: Cloning of the alpha-amylase cDNA of Aspergillus shiroyamii and its expression
A;Reference number: JS0663; MUID:92323146; PMID:1368777
A;Accession: JS0663
A;Molecule type: mRNA
A;Residues: 1-499 <SHI>
C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-499/Product: alpha-amylase #status predicted <ALP>
F;194-321/Domain: alpha-amylase core homology <AMY>
F;218/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	79.7%;	Score 397;	DB 2;	Length 499;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 497;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy 1	MVAVNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGG	60		
Db 2	MVAVNSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGGTTATCNTADQKCGG	61		
Qy 61	TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL	120		
Db 62	TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL	121		
Qy 121	KALSSALHERGMYLMDVVDVVAHMGYDGGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ	180		
Db 122	KALSSALHERGMYLMDVVDVVAHMGYDGGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ	181		
Qy 181	VEDCWLGNTVSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPFGYN	240		
Db 182	VEDCWLGNTVSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDFWPFGYN	241		
Qy 241	KAAGVYCIGEVLDGDPATCTPQNVMDGVLNPIYIYPLLNAPKSTGSMDDLNNMINTVK	300		
Db 242	KAAGVYCIGEVLDGDPATCTPQNVMDGVLNPIYIYPLLNAPKSTGSMDDLNNMINTVK	301		
Qy 301	SDCPDSTLLGTFFVENHNDPRFASVTNDIALAKNVAFAFIILNDGIPILYAGQEQHYAGGND	360		
Db 302	SDCPDSTLLGTFFVENHNDPRFASVTNDIALAKNVAFAFIILNDGIPILYAGQEQHYAGGND	361		
Qy 361	PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKKNWPIYKDDTTIAMRKGT	420		
Db 362	PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFTVYKKNWPIYKDDTTIAMRKGT	421		
Qy 421	DGSOQVITILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTGTGSDGNVPVPMAGGLP	480		
Db 422	DGSOQVITILSNKGASGDSYTLISLGSAGYTAGQQLTEVIGCTTGTGSDGNVPVPMAGGLP	481		
Qy 481	RVLYPTEKLAGSKICSSS 498			
Db 482	RVLYPTEKLAGSKICSSS 499			

RESULT 3
A48305
alpha-amylase (EC 3.2.1.1) A precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A48305
R;Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A;Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper
A;Reference number: A48305; MUID:90254827; PMID:2340591
A;Accession: A48305
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-498 <KOR>
A;Cross-references: UNIPROT:Q02905
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;194-321/Domain: alpha-amylase core homology <AMY>

Query Match	77.1%;	Score 384;	DB 2;	Length 498;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGGSTTATCNTADQKCGG 60
DB 2 MYAWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGGSTTATCNTADQKCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL 121
QY 121 KALSALHERGMVLMVDVNVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSALHERGMVLMVDVNVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241
QY 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDDLYNMINTVK 300
DB 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDDLYNMINTVK 301
QY 301 SDCPDSTLLGTFFVENHNDPRFASVTNDIALAKNVAAFIILNDGIPITIIYAGQSOHYAGGND 360
DB 302 SDCPDSTLLGTFFVENHNDPRFASVTNDIALAKNVAAFIILNDGIPITIIYAGQSOHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 4
B48305
alpha-amylase (EC 3.2.1.1) B precursor - Aspergillus awamori
C:Species: Aspergillus awamori
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: B48305
R:Korman, D.R.; Bayliss, F.T.; Barnett, C.C.; Carmona, C.L.; Kodama, K.H.; Royer, T.J.;
Curr. Genet. 17, 203-212, 1990
A:Title: Cloning, characterization, and expression of two alpha-amylase genes from Asper
A:Reference number: A48305; MUID:90254827; PMID:2340591
A:Accession: B48305
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-499 <KOR>
A:Cross-references: UNIPROT:Q02906
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:194-321/Domain: alpha-amylase core homology <AMY>

Query Match 77.1%; Score 384; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGGSTTATCNTADQKCGG 60
DB 2 MYAWSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGGSTTATCNTADQKCGG 61
QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENYGTADDL 121
QY 121 KALSALHERGMVLMVDVNVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 180
DB 122 KALSALHERGMVLMVDVNVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQ 181
QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241

QY 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDDLYNMINTVK 300
DB 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDDLYNMINTVK 301
QY 301 SDCPDSTLLGTFFVENHNDPRFASVTNDIALAKNVAAFIILNDGIPITIIYAGQSOHYAGGND 360
DB 302 SDCPDSTLLGTFFVENHNDPRFASVTNDIALAKNVAAFIILNDGIPITIIYAGQSOHYAGGND 361
QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 5
ALAS3
alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae
N:Alternate names: alpha-amylase isozyme I; glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S04549; A33215; A44713
R:Witschel, S.; Lachmund, A.; Wildhardt, G.; Ruttkowski, E.
Mol. Microbiol. 3, 3-14, 1989
A:Title: Three alpha-amylase genes of Aspergillus oryzae exhibit identical intron-exon
A:Reference number: S04548; MUID:89237897; PMID:2785629
A:Accession: S04549
A:Molecule type: DNA
A:Residues: 1-499 <WIR>
A:Cross-references: UNIPROT:Q96TH4; EMBL:X12727; NID:g2454; PIDN:CAA31220.1; PID:g29592.
A:Accession: A33215
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-499 <WI2>
A:Cross-references: GB:X12727; NID:g2454; PIDN:CAA31220.1; PID:g295922
R:Genes, M.J.; Dove, M.J.; Seligy, V.L.
Gene 79, 107-117, 1989
A:Title: Aspergillus oryzae has two nearly identical Taka-amylase genes, each containin
A:Reference number: J50240; MUID:89378767; PMID:2789162
A:Accession: A44713
A:Molecule type: DNA
A:Residues: 1-499 <GEN>
A:Note: the authors refer to this as isozyme I
R:Matsumura, Y.; Kusunoki, M.; Harada, W.; Kakudo, M.
J. Biochem. 95, 697-702, 1984
A:Title: Structure and possible catalytic residues of Taka-amylase A.
A:Reference number: A37454; MUID:84212370; PMID:6609921
A:Contents: annotation; X-ray crystallography, 3.0 angstroms
C:Comment: One atom of calcium per molecule is essential for activity.
C:Genetics:
A:Gene: amy3; Amy1
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: calcium; carbohydrate digestion; glycoprotein; glycosidase; hydrolase; meta
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-499/Product: alpha-amylase 3 #status experimental <MAT>
F:194-321/Domain: alpha-amylase core homology <AMY>
F:51-59,171-185,261-304,461-496/Disulfide bonds: #status experimental
F:142,183,196,231/Binding site: calcium (Asn, Glu, Asp, His) #status predicted
F:218/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:231,251,318/Active site: His, Glu, Asp #status experimental

Query Match 68.7%; Score 342; DB 1; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 KYCGGTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENY 115
DB 57 KYCGGTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDVGHYQWQDIYSLNENY 116
QY 116 TADDLKALSSALHERGMVLMVDVNVANHMGVDGAGSSVDYSVFKPFSSQDYFHPFCFIQNY 175

Db	117	TADDLKALSSALHERGMYLWVDVANHMGYDAGSSVDYSVPKPFSSQDYFHPFCLIQNY	176
Qy	176	EDQTOVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKRVQKDF	235
Db	177	EDQTOVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKRVQKDF	236
Qy	236	WFGYNKAAGVYICIGEVLDGDPAYTCYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDLLNM	295
Db	237	WFGYNKAAGVYICIGEVLDGDPAYTCYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDLLNM	296
Qy	296	INTVKSDDPDSLLGTGFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEORH	355
Db	297	INTVKSDDPDSLLGTGFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEORH	356
Qy	356	AGGNDPANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIA	415
Db	357	AGGNDPANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIA	416
Qy	416	MRKGTGSGQIVTILSNKGASGDSYTLISGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPM	475
Db	417	MRKGTGSGQIVTILSNKGASGDSYTLISGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPM	476
Qy	476	AGGLPRVLYPTEKLAGSKICSSS	498
Db	477	AGGLPRVLYPTEKLAGSKICSSS	499
RESULT 6			
JN0588			
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae			
N:Alternate names: Taka-amylase A			
C:Species: Aspergillus oryzae			
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004			
C:Accession: JN0588			
R:Tsukagoshi, N.; Furukawa, M.; Nagaba, H.; Kirita, N.; Tsuboi, A.; Udaka, S.			
Gene 84, 319-327, 1989			
A:Title: Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A: evidence for mu			
A:Reference number: JN0588; MUID:90128276; PMID:5612911			
A:Accession: JN0588			
A:Molecule type: mRNA			
A:Residues: 1-499 <TSU>			
A:Cross-references: UNIPROT:Q96TH4			
C:Comment: The alpha amylases are encoded by multigene family.			
C:Genetics:			
A:Gene: Taa-G1			
A:Introns: 56/1; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3			
C:Function:			
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds			
A:Pathway: glycogen/starch degradation			
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology			
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation			
F:1-21/Domain: signal sequence #status predicted <SIG>			
F:124-499/Product: alpha-amylase #status predicted <WAT>			
F:194-321/Domain: alpha-amylase core homology <AMY>			
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Query Match 59.4%; Score 296; DB 2; Length 499;			
Best Local Similarity 99.6%; Pred. No. 3.8e-294;			
Matches 496; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	MVAMWSFLYGLQVAAPALATPADWRQSIFVLLTDRFARTDGSSTTATCNTADQKCGG	60
Db	2	MVAMWSFLYGLQVAAPALATPADWRQSIFVLLTDRFARTDGSSTTATCNTADQKCGG	61
Qy	61	TWQGIIDKLDYIQMGFTAIWITPTAQLPQTAYGDAYHGWQDIYSLNENYGTADDL	120
Db	62	TWQGIIDKLDYIQMGFTAIWITPTAQLPQTAYGDAYHGWQDIYSLNENYGTADDL	121
Qy	121	KALSSALHERGMYLMVDVANHMGYDAGSSVDYSVPKPFSSQDYFHPFCLIQNYEDQTO	180
Db	122	KALSSALHERGMYLMVDVANHMGYDAGSSVDYSVPKPFSSQDYFHPFCLIQNYEDQTO	181

Qy	181	VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKRVQKDFWPGYN	240
Db	182	VEDCWLGDNTVSLPDLDTTKDVVKNEWYDWGSLVSNYSIDGLRIDTVKRVQKDFWPGYN	241
Qy	241	KAAGVYICIGEVLDGDPAYTCYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDLLNMINTVK	300
Db	242	KAAGVYICIGEVLDGDPAYTCYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDLLNMINTVK	301
Qy	301	SDCPDSTLLGTGFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEORHAGND	360
Db	302	SDCPDSTLLGTGFVENHNDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEORHAGND	361
Qy	361	PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKT	420
Db	362	PANREATWLSGYPTDSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKT	421
Qy	421	DGSIQIVTILSNKGASGDSYTLISGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP	480
Db	422	DGSIQIVTILSNKGASGDSYTLISGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP	481
Qy	481	RVLYPTEKLAGSKICSSS	498
Db	482	RVLYPTEKLAGSKICSSS	499
RESULT 7			
JN0466			
alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae			
N:Alternate names: glycogenase; Taka-amylase A			
C:Species: Aspergillus oryzae			
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004			
C:Accession: JN0466			
R:Tada, S.; Imura, Y.; Gomi, K.; Takahashi, K.; Hara, S.; Yoshizawa, K.			
Agric. Biol. Chem. 53, 593-599, 1989			
A:Title: Cloning and nucleotide sequence of the genomic Taka-amylase A gene of Aspergill			
A:Reference number: JN0466			
A:Accession: JN0466			
A:Molecule type: DNA			
A:Residues: 1-499 <TAD>			
A:Cross-references: UNIPROT:P10529			
C:Comment: See also PIR:JK0201 and PIR:JS0240.			
C:Comment: One atom of calcium per molecule is essential for activity.			
C:Genetics:			
A:Introns: 56/3; 69/3; 108/2; 144/3; 221/1; 275/2; 324/2; 404/3			
C:Function:			
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds			
A:Pathway: glycogen/starch degradation			
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology			
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation			
F:1-21/Domain: signal sequence #status predicted <SIG>			
F:22-499/Product: alpha-amylase #status predicted <WAT>			
F:194-321/Domain: alpha-amylase core homology <AMY>			
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted			
F:231,251,318/Active site: His, Glu, Asp #status predicted			
Query Match 49.0%; Score 244; DB 2; Length 499;			
Best Local Similarity 100.0%; Pred. No. 5.7e-241;			
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	255	DPAYTCYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDLLNMINTVKSDCPDSTLLGTFFVE	314
Db	256	DPAYTCYQNVMDGVLNPIYIYPLLNAPFKSTSGSMDLLNMINTVKSDCPDSTLLGTFFVE	315
Qy	315	NHDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEORHAGNDPANREATWLSGYPT	374
Db	316	NHDNPRFASVTNDIALAKNVAAPFIILNDGIPPIYAGOEORHAGNDPANREATWLSGYPT	375
Qy	375	DSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKTGDSQIVTILSNKGA	434
Db	376	DSELYKLIASANAIRNVAISKDTGFVYKNWPIYKDDTTIAMRKTGDSQIVTILSNKGA	435
Qy	435	SGDSYTLISGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLPRVLYPTEKLAGSKI	494

Db 436 SGDSYTLISGAGYTAGQQLTEVIGCTTTVSGDGNVPVPMAGGLPRVLPTTEKLAGSKI 495
QY 495 CSSS 498
|||||
Db 496 CSSS 499
|||||
RESULT 8
JK0201
alpha-amylase (EC 3.2.1.1) - Aspergillus oryzae
N:Alternate names: glycogenase; Taka-amylase A
C:Species: Aspergillus oryzae
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: JK0201
R:Toda, H.; Kondo, K.; Narita, K.
Proc. Jpn. Acad. 58B, 208-212, 1982
A:Title: The complete amino acid sequence of Taka-amylase A.
A:Reference number: JK0201
A:Accession: JK0201
A:Molecule type: protein
A:Residues: 1-478 <TOD>
A:Cross-references: UNIPROT:P10529
C:Comment: One atom of calcium per molecule is essential for the activity.
C:Comment: This enzyme is a glycoprotein.
C:Comment: See also PIR:J70466 and PIR:J50240.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domain: alpha-amylase core homology <AMY>
F:197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:210,230,297/Active site: His, Glu, Asp #status experimental
Query Match 47.8%; Score 238; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 7.6e-235;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 106 DIYSLNENYGTADDKALSSALHERGMYLMVDVNVANHMGYDGGSSVDYVFKPSSQDY 165
Db 86 DIYSLNENYGTADDKALSSALHERGMYLMVDVNVANHMGYDGGSSVDYVFKPSSQDY 145
QY 166 FHPFCFIQNYEQTVQVEDCWLGDNTVSLPDLTTKDVKNVNEWYDVGSLVSNYSIDGLRI 225
Db 146 FHPFCFIQNYEQTVQVEDCWLGDNTVSLPDLTTKDVKNVNEWYDVGSLVSNYSIDGLRI 205
QY 226 DTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPATVCPYQNVMDGVNLNPIYYPLLNAFKST 285
Db 206 DTVKHVQKDFWPGYNKAAGVYICIGEVLDGDPATVCPYQNVMDGVNLNPIYYPLLNAFKST 265
QY 286 SGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASVTNDIALAKNVAAFIILNDG 343
Db 266 SGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASVTNDIALAKNVAAFIILNDG 323
RESULT 9
S33921
alpha-amylase (EC 3.2.1.1) SWA2 precursor - yeast (Schwanniomyces occidentalis)
N:Alternate names: alpha-1,4 glucanohydrolase
C:Species: Schwanniomyces occidentalis
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S33921
R:Claros, M.G.; Abarca, D.; Fernandez-Lobato, M.; Jimenez, A.
Curr. Genet. 24, 75-83, 1993
A:Title: Molecular structure of the SWA2 gene encoding an AMY1-related alpha-amylase from
A:Reference number: S33921; MUID:93365041; PMID:8358835
A:Accession: S33921
A:Molecule type: DNA
A:Residues: 1-507 <CLA>
A:Cross-references: UNIPROT:Q08806; EMBL:X73497; NID:g396561; PIDN:CAA51912.1; PID:g3965
C:Genetics:
A:Gene: SWA2
C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-507/Product: alpha-amylase #status predicted <MAT>
F:205-332/Domain: alpha-amylase core homology <AMY>
F:134,229/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 4.0%; Score 20; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 7.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 63 QGIIDKLDYIQGMGFTAIWI 82
Db 75 QGIIDKLDYIQGMGFTAIWI 94
RESULT 10
S23355
alpha-amylase (EC 3.2.1.1) precursor - yeast (Schwanniomyces occidentalis)
C:Species: Schwanniomyces occidentalis
C>Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S23355
R:Wu, F.M.; Wang, T.T.; Heu, W.H.
FEMS Microbiol. Lett. 82, 313-318, 1991
A:Title: The nucleotide sequence of Schwanniomyces occidentalis alpha-amylase gene.
A:Reference number: S23355
A:Accession: S23355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <WUF>
A:Cross-references: UNIPROT:P19269; EMBL:X62079; NID:g4880; PIDN:CAA33995.1; PID:g4881
A:Note: The authors translated the codon AGA for residue 21 as Pro, CTT for residue 61
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase
F:209-336/Domain: alpha-amylase core homology <AMY>
Query Match 3.8%; Score 19; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64 GIIDKLDYIQGMGFTAIWI 82
Db 80 GIIDKLDYIQGMGFTAIWI 98
RESULT 11
S06115
alpha-amylase (EC 3.2.1.1) AMY1 precursor - yeast (Schwanniomyces occidentalis)
C:Species: Schwanniomyces occidentalis
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: S06115
R:Strasser, A.W.M.; Selk, R.; Dohmen, R.J.; Niermann, T.; Bielefeld, M.; Seeboth, P.; T.
Eur. J. Biochem. 184, 699-706, 1989
A:Title: Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the sec
A:Reference number: S06115; MUID:90032659; PMID:2806251
A:Accession: S06115
A:Molecule type: DNA
A:Residues: 1-512 <STR>
A:Cross-references: UNIPROT:P19269; EMBL:X16040; NID:g4882; PIDN:CAA34162.1; PID:g4883
C:Genetics:
A:Gene: AMY1
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-512/Product: alpha-amylase #status predicted <MAT>
F:209-336/Domain: alpha-amylase core homology <AMY>
Query Match 3.8%; Score 19; DB 2; Length 512;

Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GIIDKLDYIQGMGFTAIWI 82
|||||
DB 80 GIIDKLDYIQGMGFTAIWI 98
|||||

RESULT 12
T38770
alpha-amylase a precursor - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38770
R:Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21751
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T38770
A:Molecule type: DNA
A:Residues: 1-513 <SKS>
A:Cross-references: UNIPROT:O14154; EMBL:Z98762; PIDN:CAM11471.1; GSPDB:GN00066; SPDB:SE
A:Experimental source: strain 972h-; cosmid c4A8
C:Genetics:
A:Gene: SPDB:SPAC4A8.01
A:Map position: 1
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology

Query Match 3.8%; Score 19; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 7.9e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 GIIDKLDYIQGMGFTAIWI 82
|||||
DB 66 GIIDKLDYIQGMGFTAIWI 84
|||||

RESULT 13
JC4510
pullulanase (EC 3.2.1.41) precursor - yeast (Lipomyces kononenkoae)
N:Alternate names: LKA1 protein; raw starch-degrading amylase
N:Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C:Species: Lipomyces kononenkoae
C:Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4510; PC4116
R:Steyn, A.D.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A:Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lip
A:Reference number: JC4510; MUID:96105202; PMID:8529895
A:Molecule type: mRNA
A:Accession: JC4510
A:Residues: 1-624 <STB>
A:Cross-references: UNIPROT:Q01117; GB:U03076; NID:g1173536; PIDN:AAC49622.1; PID:g11735
A:Experimental source: strain IGC4052B
A:Accession: PC4116
A:Molecule type: protein
A:Residues: 29-44 <ST>
A:Experimental source: IGC4052B
C:Genetics:
A:Gene: LKA1
C:Function:
A:Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
A:Pathway: glycogen/starch degradation
C:Superfamily: Lipomyces alpha-amylase; alpha-amylase core homology; glucoamylase starch
C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-624/Product: alpha-amylase #status predicted <MAT>
F:48-141/Domain: Glucoamylase starch-binding domain homology <SBD>
F:320-447/Domain: alpha-amylase core homology <AMY>
F:177-185,297-311,387-430,587-622/Disulfide bonds: #status predicted
F:304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 3.2%; Score 16; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 NYSIDGLRIDTVKRVQ 232
|||||
DB 344 NYSIDGLRIDTVKRVQ 359
|||||

RESULT 14
A35282
alpha-amylase (EC 3.2.1.1) - Aspergillus niger
C:Species: Aspergillus niger
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A35282
R:Boel, E.; Brady, L.; Brzozowski, A.M.; Derewenda, Z.; Dodson, G.G.; Jensen, V.J.; Pete
Biochemistry 29, 6244-6249, 1990
A:Title: Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-angstrom r
A:Reference number: A35282; MUID:91002514; PMID:2207069
A:Accession: A35282
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-484 <BOB>
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:173-300/Domain: alpha-amylase core homology <AMY>

Query Match 2.8%; Score 14; DB 1; Length 484;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 LDYIQGMGFTAIWI 82
|||||
DB 49 LDYIQGMGFTAIWI 62
|||||

RESULT 15
S31478
alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris
C:Species: Thermoactinomyces vulgaris
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S31478
R:Hofemeister, B.; Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; Hansen, G.; H
submitted to the EMBL Data Library, December 1992
A:Description: The gene amyTV coding for a non-glucogenic alpha-amylase from Thermoactin
A:Reference number: S31478
A:Accession: S31478
A:Molecule type: DNA
A:Residues: 1-482 <HOP>
A:Cross-references: UNIPROT:Q60051; EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g48290
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:194-319/Domain: alpha-amylase core homology <AMY>

Query Match 2.4%; Score 12; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 MGFTAIWITPVT 86
|||||
DB 89 MGFTAIWITPVT 100
|||||

Search completed: November 7, 2005, 19:33:47
Job time : 62.5676 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 19:00:20 ; Search time 264.382 Seconds
(without alignments)
964.571 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
Sequence: 1 MVAWWSFLYGLQVAAPALA.....LPRVLVPTPEKLAKSGKICSSS 498

Scoring table:
Oligo Gap 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_eprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	498	2 Q76CT3	Q76ct3 aspergillus
2	498	100.0	499	1 AMYA_ASPOR	P10529 aspergillus
3	397	79.7	499	1 AMY_ASPSH	P30292 aspergillus
4	397	79.7	499	2 Q76L99	Q76l99 aspergillus
5	384	77.1	498	1 AMYA_ASPAW	Q02305 aspergillus
6	384	77.1	499	1 AMYB_ASPAW	Q02306 aspergillus
7	342	68.7	499	2 Q96TH4	Q96th4 aspergillus
8	342	68.7	499	2 Q71LV45	Q71lv45 aspergillus
9	23	4.6	623	2 Q9UV09	Q9uv09 emericella
10	20	4.0	507	1 AMY2_DREBOC	Q08806 debaryomyce
11	19	3.8	490	2 Q9UV07	Q9uv07 emericella
12	19	3.8	512	1 AMY1_DREBOC	P19269 debaryomyce
13	19	3.8	513	1 AMY3_SCHPO	O14154 schizosacch
14	16	3.2	624	1 AMY1_LIPKO	Q01117 lipomyces k
15	16	3.2	647	2 Q6VF33	Q6vf33 lipomyces s
16	14	2.8	634	2 Q76L96	Q76l96 aspergillus
17	14	2.8	640	2 O13296	O13296 aspergillus
18	12	2.4	482	2 Q60051	Q60051 thermoactin
19	12	2.4	492	2 Q7SDJ6	Q7sdj6 neurospora
20	12	2.4	1196	1 AMYB_PABPO	P21543 paenibacill
21	11	2.2	484	1 AMYA_ASPNG	P56271 aspergillus
22	11	2.2	494	1 AMY1_SACFI	P21567 saccharomyc
23	10	2.0	128	2 O15751	O15751 dictyosatel
24	10	2.0	533	2 Q7S4K0	Q7s4k0 neurospora
25	10	2.0	621	2 Q74922	Q74922 schizosacch
26	10	2.0	631	2 Q92394	Q92394 cryptococcu
27	9	1.8	90	2 Q651X5	Q651x5 oryza sativ
28	9	1.8	199	2 Q7VXM8	Q7vxm8 bordetella
29	9	1.8	225	2 Q7WI40	Q7wi40 bordetella
30	9	1.8	229	2 Q7W674	Q7w674 bordetella
31	9	1.8	421	2 Q82BV7	Q82bv7 streptomyce

32	9	1.8	454	2 Q8EFW1	Q8efw1 xanthomonas
33	9	1.8	581	1 AMY1_SCHPO	Q09840 schizosacch
34	9	1.8	1021	2 Q9K5L6	Q9k5l6 actinoplan
35	9	1.8	1291	2 Q67TF1	Q67tf1 symbiobacte
36	8	1.6	88	2 Q6YI86	Q6yi86 staphylococ
37	8	1.6	105	2 Q94DD3	Q94dd3 oryza sativ
38	8	1.6	140	2 Q9RTS9	Q9rts9 deinococcus
39	8	1.6	149	2 Q9AAF1	Q9aaf1 caulobacter
40	8	1.6	151	2 Q9CI07	Q9ci07 lactococcus
41	8	1.6	156	1 C055_ARADI	P80518 araneus dia
42	8	1.6	157	2 Q8NXR1	Q8nxr1 staphylococ
43	8	1.6	157	2 Q6GBG0	Q6gbg0 staphylococ
44	8	1.6	157	2 Q6GJ01	Q6gj01 staphylococ
45	8	1.6	160	2 Q9Y9S9	Q9y9s9 aeropyrum p

ALIGNMENTS

RESULT 1

Q76CT3 PRELIMINARY; PRT; 498 AA.

AC Q76CT3; 05-JUL-2004 (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE Alpha-amyase.

GN Name=amyA;

OS Aspergillus kawachi (Aspergillus awamori var. kawachi).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OC NCBI_TaxID=40384;

RN [1]

RP SEQUENCE FROM N.A.

RA Ito K.;

RL Submitted (MAY-2003) to the EMBL/Genbank/DBJ databases.

CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

DR EMBL; AB109452; BAD01051.1; -.

DR GO; GO:0004556; F:alpha-amyase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; Alpha-amyase; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

DR SMART; SM00642; Aamy; 1.

SQ SEQUENCE 498 AA; 54679 MW; 8407BBFC7E4E3FC0 CRC64;

Query Match 100.0%; Score 498; DB 2; Length 498;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAWWSFLYGLQVAAPALAATPADWRSQSIYFLLTDFRFTDGTGTTATCNTADQKCGG 60

Db 1 MVAWWSFLYGLQVAAPALAATPADWRSQSIYFLLTDFRFTDGTGTTATCNTADQKCGG 60

QY 61 TWQGIIDKLDYIQGMGFTAINITPVTAQLPQTAYGDAVHYGWQDDIYSLNENYGTDLL 120

Db 61 TWQGIIDKLDYIQGMGFTAINITPVTAQLPQTAYGDAVHYGWQDDIYSLNENYGTDLL 120

QY 121 KALSALLHERGMYLMVDVNVANHMGVDGAGSSYDYSVFKPFSSQDYFHPFCFTQNYEDQTK 180

Db 121 KALSALLHERGMYLMVDVNVANHMGVDGAGSSYDYSVFKPFSSQDYFHPFCFTQNYEDQTK 180

QY 181 VEDCVLGNTVSLPDLTTDKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240

Db 181 VEDCVLGNTVSLPDLTTDKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVKQDFWPGYN 240

QY 241 KAAGVYICGEVLGDGPAYTCPYQNVMDGVLYNPIYYPPLNFAFKSTGSGMDDLNNMINTVK 300

Db 241 KAAGVYICGEVLGDGPAYTCPYQNVMDGVLYNPIYYPPLNFAFKSTGSGMDDLNNMINTVK 300

QY 301 SDCPDSTLLGTFTVENHNDPRFASNTNDIALAKNVAFIINDGIPPIYAGQEQHAGGND 360

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|||||
301 SDCPDSTLLGTEVENHNDPRFASVTNDIALAKNVAFIILNDGIPILVAGQSQHVAGND 360
|||||
361 PANREATWLSGYPTDSSELYKLTASANAIRNYAISKDTGVTYKKNWPIYKDDTTIAMRGT 420
|||||
361 PANREATWLSGYPTDSSELYKLTASANAIRNYAISKDTGVTYKKNWPIYKDDTTIAMRGT 420
|||||
421 DGSQVITVILSNKGASGDSYTLISLSGAGYTAGOOLTEVIGCTTGTGSDGNVPPVWAGGLP 480
|||||
421 DGSQVITVILSNKGASGDSYTLISLSGAGYTAGOOLTEVIGCTTGTGSDGNVPPVWAGGLP 480
|||||
481 RVLYPTEKLAGSKICSSS 498
|||||
481 RVLYPTEKLAGSKICSSS 498

RESULT 2
AMYA ASPOR
ID AMYA ASPOR STANDARD; PRT; 499 AA.
AC P10529; P11763; Q00250;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (Taka-amylase A) (TAA) (1,4-
DE alpha-D-glucan glucanohydrolase).
GN Name=AMY1;
GN and
GN Name=AMY2;
GN and
GN Name=AMY3;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 63303;
RX MEDLINE=89237897; PubMed=2785629;
RA Wiesel S., Lachmund A., Wildhardt G., Rutkowski E.;
RT "Three alpha-amylase genes of Aspergillus oryzae exhibit identical
RT intron-exon organization.";
RL Mol. Microbiol. 3:3-14(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89378767; PubMed=2789162; DOI=10.1016/0378-1119(89)90096-6;
RA Genes M.J., Dove M.J., Seligy V.L.;
RT "Aspergillus oryzae has two nearly identical Taka-amylase genes, each
RT containing eight introns.";
RL Gene 79:107-117(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Tada S., Iimura Y., Gomi K., Takahashi K., Hara S., Yoshizawa K.;
RT "Cloning and nucleotide sequence of the genomic Taka-amylase A gene of
RT Aspergillus oryzae.";
RL Agric. Biol. Chem. 53:593-599(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128276; PubMed=2612911; DOI=10.1016/0378-1119(89)90506-4;
RA Tsukagoshi N., Furukawa M., Nagaba H., Kirita N., Tsuboi A., Udaoka S.;
RT "Isolation of a cDNA encoding Aspergillus oryzae Taka-amylase A:
RT evidence for multiple related genes.";
RL Gene 84:319-327(1989).
RN [5]
RP SEQUENCE OF 22-499.
RA Toda H., Kondo K., Narita K.;
RT "The complete amino acid sequence of Taka-amylase A.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 58:208-212(1982).
RN [6]
RP SEQUENCE OF 206-225.
RX MEDLINE=74001521; PubMed=4733850;
RA Isemura S., Ikenaka T.;
RT "The amino acid sequences of glycopeptides obtained from Taka-amylase
RT A with trypsin and chymotrypsin.";

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J. Biochem. 74:1-10(1973).
RN [7]
RP SEQUENCE OF 433-499.
RA Narita K.;
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 51:285-290(1975).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=80227691; PubMed=6156152;
RA Matsuura Y., Kusunoki M., Harada W., Tanaka N., Iga Y., Yasuoka N.,
RA Toda H., Narita K., Kakudo M.;
RT "Molecular structure of taka-amylase A. I. Backbone chain folding at
RT 3-A resolution.";
RL J. Biochem. 87:1555-1558(1980).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
RX MEDLINE=84212370; PubMed=6609921;
RA Matsuura Y., Kusunoki M., Harada W., Kakudo M.;
RT "Structure and possible catalytic residues of Taka-amylase A.";
RL J. Biochem. 95:697-702(1984).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=97428212; PubMed=9283074; DOI=10.1021/bi970539i;
RA Brzowski A.M., Davies G.J.;
RT "Structure of the Aspergillus oryzae alpha-amylase complexed with the
RT inhibitor acarbose at 2.0-A resolution.";
RL Biochemistry 36:10837-10845(1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations.
CC -!- SUBUNIT: Monomer.
CC -!- BIOTECHNOLOGY: Used in the brewing industry to increase the
CC fermentability of beer worts (including those made from unmalted
CC cereals), in the starch industry to make high maltose and high DE
CC syrups (starch saccharification), in the alcohol industry to
CC reduce fermentation time, in the cereal food industry for flour
CC supplementation and improvement of chilled and frozen dough, and
CC in the forestry industry for low-temperature modification of
CC starch. Sold under the name Fungamyl by Novozymes.
CC -!- MISCELLANEOUS: The sequence of AMY1 and AMY2 is shown.
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X12725; CAA31218.1; -
DR EMBL; X12726; CAA31219.1; -
DR EMBL; X12727; CAA31220.1; -
DR EMBL; D00434; BAA00336.1; -
DR EMBL; M33218; AAA32708.1; -
DR PIR; JK0201; JK0201.
DR PIR; JT0466; JT0466.
DR PIR; S04548; ALAS1.
DR PDB; 2TAA; X-ray; A=22-499.
DR PDB; 6TAA; X-ray; @=22-499.
DR PDB; 7TAA; X-ray; @=22-499.
DR GlycoSuiteDB; P10529; -
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW 3D-structure; Calcium-binding; Carbohydrate metabolism;
KW Direct protein sequencing; Glycoprotein; Glycosidase; Hydrolase;
KW Multigene family; Signal.
FT SIGNAL 1 21
FT CHAIN 22 499 Alpha-amylase A.

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[illegible]

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CC EMBL; D10461; BAA01255.1; --
CC HSPF; P10529; 7TAA.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydroxylase; Signal.
FT SIGNAL 1 21
FT CHAIN 22 499 Alpha-amyase.
FT ACT_SITE 227 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).
FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (By similarity).
SQ SEQUENCE 499 AA; 54852 MW; 1FB7AE50DA01C03F CRC64;

Query Match 79.7%; Score 397; DB 1; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSITATCNTADQKCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSITATCNTADQKCGG 61

QY 61 TWQGIIDKLDYIQMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMVLDVVAHNGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
DB 122 KALSSALHERGMVLDVVAHNGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 181

QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDPWPGYN 240
DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDPWPGYN 241

QY 241 KAAGYVICGEVLGDGPAYTCYQNVMDGVNLPIYYPILLNAFKSTSGSMDDLNNINTVK 300
DB 242 KAAGYVICGEVLGDGPAYTCYQNVMDGVNLPIYYPILLNAFKSTSGSMDDLNNINTVK 301

QY 301 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPIIYAGQEHVAGND 360
DB 302 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPIIYAGQEHVAGND 361

QY 361 PANREATWLSGYPDTSSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 420
DB 362 PANREATWLSGYPDTSSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 421

QY 421 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

QY 481 RVLYPTEKLAGSKICSSS 498
DB 482 RVLYPTEKLAGSKICSSS 499

RESULT 4

Q76L99 PRELIMINARY; PRT; 499 AA.
ID Q76L99
AC Q76L99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amyase precursor.
GN Name=amyl 1;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT-11;
RA Matsubara T.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB083159; BAD06002.1; --
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
SQ SEQUENCE 499 AA; 54794 MW; 2B357AE38B36C1C2 CRC64;

Query Match 79.7%; Score 397; DB 2; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 497; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSITATCNTADQKCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGSITATCNTADQKCGG 61

QY 61 TWQGIIDKLDYIQMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQMGFTAIWITPVTAQLPQTAYGDAYHGYWQDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMVLDVVAHNGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 180
DB 122 KALSSALHERGMVLDVVAHNGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTO 181

QY 181 VEDCWLGDNTVSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDPWPGYN 240
DB 182 VEDCWLGDNTVSLPDLDTTKDVVKNWYDWGSLVSNYSIDGLRIDTVKHVKQDPWPGYN 241

QY 241 KAAGYVICGEVLGDGPAYTCYQNVMDGVNLPIYYPILLNAFKSTSGSMDDLNNINTVK 300
DB 242 KAAGYVICGEVLGDGPAYTCYQNVMDGVNLPIYYPILLNAFKSTSGSMDDLNNINTVK 301

QY 301 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPIIYAGQEHVAGND 360
DB 302 SDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAFAFIILNDGIPIIYAGQEHVAGND 361

QY 361 PANREATWLSGYPDTSSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 420
DB 362 PANREATWLSGYPDTSSELYKLIASANAIRNVAISKDTGFTVYKNWPIYKDDTTIAMRGT 421

QY 421 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 480
DB 422 DGSQIVTILSNKGASGDSYTLISLSGAGYTAGQQLTEVIGCTTIVTSGDGNVPVPMAGGLP 481

QY 481 RVLYPTEKLAGSKICSSS 498
DB 482 RVLYPTEKLAGSKICSSS 499

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RESULT 5
AMYA_ASPAW STANDARD; PRT; 498 AA.
ID AMYA_ASPAW
AC Q02905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase A).
GN Name=AMYA;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52755; CAA36966.1; -.
DR FIR; A48305; A48305.
DR HSSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLAASE.
DR SMART; SM00642; Amy; 1.
DR KEGG; 04501; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 498 Alpha-amylase A.
FT ACT_SITE 227 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).
FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 498 AA; 54880 MW; 7658511BC01A8A01 CRC64;

Query Match 77.1%; Score 384; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 6

AMYB_ASPAW

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ID AMYB_ASPAW STANDARD; PRT; 499 AA.
AC Q02906;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase B).
GN Name=AMYB;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=105351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UVK143F;
RX MEDLINE=90254827; PubMed=2340591;
RA Korman D.R., Bayliss F.T., Barnett C.C., Carmona C.L., Kodama K.H.,
RA Royer T.J., Thompson S.A., Ward M., Wilson L.J., Berka R.M.;
RT "Cloning, characterization, and expression of two alpha-amylase genes
RT from Aspergillus niger var. awamori.";
RL Curr. Genet. 17:203-212(1990).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52755; CAA36967.1; -.
DR FIR; B48305; B48305.
DR HSSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.

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DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
KW Hydrolase; Multigene family; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 499 Alpha-amylase B.
FT ACT_SITE 227 227 Nucleophile (By similarity).
FT ACT_SITE 251 251 Proton donor (By similarity).
FT ACT_SITE 318 318 By similarity.
FT METAL 142 142 Calcium 1 (By similarity).
FT METAL 183 183 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 196 196 Calcium 1 (By similarity).
FT METAL 227 227 Calcium 2 (By similarity).
FT METAL 231 231 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 251 251 Calcium 2 (By similarity).
FT DISULFID 51 59 By similarity.
FT DISULFID 171 185 By similarity.
FT DISULFID 261 304 By similarity.
FT DISULFID 461 496 By similarity.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 499 AA; 54921 MW; 740B96B1BC01A8A CRC64;

Query Match 77.1%; Score 384; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAMWSFLYGLQVAAPALAAPADWRSGSIYFLLTDRFARTDGGTTATCNTADQKCGG 60
DB 2 MVAMWSFLYGLQVAAPALAAPADWRSGSIYFLLTDRFARTDGGTTATCNTADQKCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGYWQDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGYWQDIYSLNENYGTADDL 121

QY 121 KALSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHFPCFIONYEDOTQ 180
DB 122 KALSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHFPCFIONYEDOTQ 181

QY 181 VEDCWLGNTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 240
DB 182 VEDCWLGNTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGYN 241

QY 241 KAAGYVCIGEVLDPGDPAYTCPYQNVMDGVNYPYIYPLNAPKSTSGSMDLLYNMTVK 300
DB 242 KAAGYVCIGEVLDPGDPAYTCPYQNVMDGVNYPYIYPLNAPKSTSGSMDLLYNMTVK 301

QY 301 SDPCDPTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPYIYAGQEHYAGGND 360
DB 302 SDPCDPTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPYIYAGQEHYAGGND 361

QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385
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RESULT 7

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Q96TH4
ID Q96TH4 PRELIMINARY; PRT; 499 AA.
AC Q96TH4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Taka-amylase A (EC 3.2.1.1).
GN Name=amyA;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1840;
```

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RX MEDLINE=20289310; PubMed=10830498;
RA Gomi K., Akeno T., Minetoki T., Ozeki K., Kumagai C., Okazaki N.,
RA Iimura Y.;
RT "Molecular cloning and characterization of a transcriptional activator
RT gene, amyR, involved in the amylolytic gene expression in Aspergillus
RT oryzae.";
RL Biosci. Biotechnol. Biochem. 64:816-827(2000).
CC -I- SIMILARITY; Belongs to family 13 of glycosyl hydrolases.
DR EMBL; AB021876; BAA95703.1; -.
DR PIR; JN0588; JN0588.
DR PIR; S04549; ALAS3.
DR HSSP; P10529; 7TAA.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0016738; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amiyl_cat.
DR InterPro; IPR006589; Alp_amiyl_cat_sub.
DR Pfam; PF00128; Alpha-amylase; 1_13.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 499 AA; 54804 MW; EBF42ADA71D20DA9 CRC64;

Query Match 68.7%; Score 342; DB 2; Length 499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 442; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 KYCGTGWGIIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGYWQDIYSLNENY 115
DB 57 KYCGTGWGIIIDKLDYIQGMGFTAIWTPVTAQLPQTAYGDVHYGYWQDIYSLNENY 116

QY 116 TADDLKALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHFPCFIONY 175
DB 117 TADDLKALSSALHERGMYLMDVVANHMGYDAGSSVDYSVFKPFSSQDYFHFPCFIONY 176

QY 176 EDQTVQEDCWLGNTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDF 235
DB 177 EDQTVQEDCWLGNTVSLPDLDTTKDVVKNWYDVGSLVSNYSIDGLRIDTVKHVQKDF 236

QY 236 WPGYNKAAGYVCIGEVLDPGDPAYTCPYQNVMDGVNYPYIYPLNAPKSTSGSMDLLYNM 295
DB 237 WPGYNKAAGYVCIGEVLDPGDPAYTCPYQNVMDGVNYPYIYPLNAPKSTSGSMDLLYNM 296

QY 296 INTVKSDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPYIYAGQEHY 355
DB 297 INTVKSDCPDSTLLGTFVENHNDNPRFASVTNDIALAKNVAAFIILNDGIPYIYAGQEHY 356

QY 356 AGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIA 415
DB 357 AGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIA 416

QY 416 MRKGTGDSQIVTILSNKGASGDSYTLISGAGYTAGQOLTEVIGCTTVTSGDGNVPVPM 475
DB 417 MRKGTGDSQIVTILSNKGASGDSYTLISGAGYTAGQOLTEVIGCTTVTSGDGNVPVPM 476

QY 476 AGGLPRVLYPTEKLAGSKICSSS 498
DB 477 AGGLPRVLYPTEKLAGSKICSSS 499
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RESULT 8

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Q7LV45
ID Q7LV45 PRELIMINARY; PRT; 499 AA.
AC Q7LV45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN Name=amy1;
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
```


DR SMART; SM00642; Aamy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 507 Alpha-amylase 2.
 FT ACT_SITE 238 238 Nucleophile (By similarity).
 FT ACT_SITE 262 262 Proton donor (By similarity).
 FT ACT_SITE 329 329 By similarity.
 FT METAL 153 153 Calcium 1 (By similarity).
 FT METAL 194 194 Calcium 1 (via carbonyl oxygen) (By similarity).
 FT METAL 207 207 Calcium 1 (By similarity).
 FT METAL 238 238 Calcium 2 (By similarity).
 FT METAL 242 242 Calcium 1 (via carbonyl oxygen) (By similarity).
 FT METAL 262 262 Calcium 2 (By similarity).
 FT DISULFID 62 70 By similarity.
 FT DISULFID 182 196 By similarity.
 FT DISULFID 272 315 By similarity.
 FT DISULFID 470 505 By similarity.
 FT CARBOHYD 229 229 N-linked (GlcNAc...) (Probable).
 SQ SEQUENCE 507 AA; 55966 MW; 3A562B95BD8AD63 CRC64;

Query Match 4.0%; Score 20; DB 1; Length 507;
 Best Local Similarity 100.0%; Pred. No. 1.7e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 QGIIDKLDYIQMGFTAIWI 82
 |||||

Db 75 QGIIDKLDYIQMGFTAIWI 94
 |||||

RESULT 11

Q9UV07 PRELIMINARY; PRT; 490 AA.
 AC Q9UV07;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-amylase AMYA.
 GN Name=amyA;
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boase N.A., Murphy R.M., Kelly J.M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 DR EMBL; AF208225; AAF17103.1; -.
 DR HSSP; P10329; 7TAA.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006589; Alpha_aml cat.
 DR InterPro; IPR006589; Alp_aml_cat_sub.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Aamy; 1.
 SQ SEQUENCE 490 AA; 54249 MW; A891C4ACEABE5305 CRC64;

Query Match 3.8%; Score 19; DB 2; Length 490;
 Best Local Similarity 100.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 LDYIQMGFTAIWIPTVA 87
 |||||

Db 63 LDYIQMGFTAIWIPTVA 81
 |||||

RESULT 12

AMY1_DEBOC

ID AMY1_DEBOC STANDARD; PRT; 512 AA.
 AC P19259;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase 1).
 GN Name=AMY1.
 OS Debaryomyces occidentalis (Yeast) (Schwanniomyces occidentalis).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
 OX NCBI_TaxID=27300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 26076;
 RX MEDLINE=90032659; PubMed=2806251;
 RA Strasser A.W.M., Selk R., Dohmen R.J., Niermann T., Bielefeld M., Seeboth P., Tu G., Hollenberg C.P.;
 RT "Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the secretion of its gene product in transformants of different yeast genera.";
 RT Eur. J. Biochem. 184:699-706(1989).
 RL [2]
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCRC 21164;
 RX MEDLINE=92120467; PubMed=1769525; DOI=10.1016/0378-1097(91)90280-N;
 RA Wu F.M., Wang T.T., Hsu W.H.;
 RT "The nucleotide sequence of Schwanniomyces occidentalis alpha-amylase gene.";
 RL FEMS Microbiol. Lett. 66:313-318(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 26077 / CBS 2863;
 RX MEDLINE=92307400; PubMed=1612414;
 RA Park J.C., Bai S., Tai C.Y., Chun S.B.;
 RT "Nucleotide sequence of the extracellular alpha-amylase gene in the yeast Schwanniomyces occidentalis ATCC 26077.";
 RL FEMS Microbiol. Lett. 72:17-23(1992).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
 CC -!- ENZYME REGULATION: Alpha-amylase expression underlies catabolite repression by glucose.
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC -----
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 CC -----
 DR EMBL; S7586; AAB21151.2; -.
 DR EMBL; X16040; CAA34162.1; -.
 DR EMBL; X62079; CAA43995.1; -.
 DR EMBL; S38381; AAB22383.2; -.
 DR PIR; S06115; S06115.
 DR PIR; S23355; S23355.
 DR HSSP; P10529; 7TAA.
 DR InterPro; IPR006589; Alp_aml_cat_sub.
 DR InterPro; IPR006047; Alpha_aml_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Aamy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolase; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 512 Alpha-amylase 1.
 FT ACT_SITE 242 242 Nucleophile (By similarity).
 FT ACT_SITE 266 266 Proton donor (By similarity).

FT ACT_SITE 333 By similarity.
 FT METAL 157 Calcium 1 (By similarity).
 FT METAL 198 Calcium 1 (via carbonyl oxygen) (By similarity).
 FT METAL 211 Calcium 1 (By similarity).
 FT METAL 242 Calcium 2 (By similarity).
 FT METAL 246 Calcium 1 (via carbonyl oxygen) (By similarity).
 FT METAL 266 Calcium 2 (By similarity).
 FT CARBOHYD 233 N-linked (GlcNAc...) (Probable).
 FT DISULFID 66 By similarity.
 FT DISULFID 196 By similarity.
 FT DISULFID 276 By similarity.
 FT DISULFID 475 By similarity.
 FT VARIANT 32 M -> K (in strain CCRC 21164 and strain ATCC 26077).
 FT VARIANT 36 S -> G (in strain CCRC 21164).
 FT VARIANT 73 Y -> I (in strain ATCC 26077).
 FT VARIANT 280 N -> S (in strain CCRC 21164).
 FT VARIANT 350 D -> A (in strain CCRC 21164 and strain ATCC 26077).
 FT VARIANT 479 L -> S (in strain CCRC 21164 and strain ATCC 26077).
 FT VARIANT 483 S -> F (in strain CCRC 21164).
 FT SEQUENCE 512 AA; 56527 MW; 857552B2CF60F965 CRC64;
 SQ
 Query Match 3.8%; Score 19; DB 1; Length 512;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 64 GIIDKLDYIQGMGFTAIWI 82
 DB 80 GIIDKLDYIQGMGFTAIWI 98
 RESULT 13
 AMY3 SCHPO STANDARD; PRT; 513 AA.
 AC O14154; Q874R5; Q96WR6;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 25-OCT-2004 (Rel. 36, Last annotation update)
 DE Probable alpha-amylase meu30 precursor (SC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Meiotic expression up-regulated protein 30).
 GN Name=me5; Synonyms=meu30; ORFNames=SPAC25H1.09, SPAC4A8.01;
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Guilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkart G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer C., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Leinhardt R., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaou V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:1871-880(2002).
 RN [2]
 RP SEQUENCE OF 191-513 FROM N.A.
 RC STRAIN=CD16-1;
 RX MEDLINE=21270454; PubMed=11376151; DOI=10.1093/nar/29.11.2327;
 RA Watanabe T., Miyashita K., Saico T.T., Yoneki T., Kakiyama Y., Nabeshima K., Kishi Y.A., Shimoda C., Nojima H.;
 RT "Comprehensive isolation of meiosis-specific genes identifies novel proteins and unusual non-coding transcripts in Schizosaccharomyces pombe";
 RL Nucleic Acids Res. 29:2327-2337(2001).
 CC -1-CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1-COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory at high concentrations (By similarity).
 CC -1-SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
 DR EMBL; Z98762; CAB11471.1; -;
 DR EMBL; Z98944; CAD62442.1; -;
 DR EMBL; AB054314; BAB60880.1; -;
 DR PIR; T38770; T38770.
 DR HSP; P10529; 7TAA.
 DR GenedB SPombe; SPAC25H1.09; -;
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR Pfam; PF00128; Alpha-amylase; 1.
 DR SMART; SM00642; Aamy; 1.
 KW Calcium-binding; Carbohydrate metabolism; Glycoprotein; Glycosidase;
 KW Hydrolyase; Meiosis; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 513 Probable alpha-amylase meu30.
 FT ACT_SITE 226 226 Nucleophile (By similarity).
 FT ACT_SITE 250 250 Proton donor (By similarity).
 FT ACT_SITE 318 318 By similarity.
 FT METAL 143 143 Calcium 1 (By similarity).
 FT METAL 182 182 Calcium 1 (via carbonyl oxygen) (By similarity).
 FT METAL 195 195 Calcium 1 (By similarity).
 FT METAL 226 226 Calcium 2 (By similarity).
 FT METAL 230 230 Calcium 1 (via carbonyl oxygen) (By similarity).
 FT METAL 250 250 Calcium 2 (By similarity).
 FT DISULFID 52 60 By similarity.
 FT DISULFID 171 184 By similarity.
 FT DISULFID 260 304 By similarity.
 FT DISULFID 454 488 By similarity.
 FT CARBOHYD 162 162 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 357 357 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 513 AA; 58715 MW; 455DD97FA428C182 CRC64;
 Query Match 3.8%; Score 19; DB 1; Length 513;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 64 GIIDKLDYIQGMGFTAIWI 82
 DB 66 GIIDKLDYIQGMGFTAIWI 84

```
RESULT 14
AMYL_LIPKO STANDARD; PRT; 624 AA.
AC Q01117;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase 1 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase 1).
GN Name=LKAl;
OS Lipomyces kononenkoae.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Lipomycetaceae; Lipomyces.
OX NCBI_TaxID=34357;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IGC4052B;
RX MEDLINE=96105202; PubMed=8529895; DOI=10.1016/0378-1119(95)00633-0;
RA Steyn A.J.C., Marmur J., Pretorius I.S.;
RT "Cloning, sequence analysis and expression in yeasts of a cDNA
RT containing a Lipomyces kononenkoae alpha-amylase-encoding gene.";
RL Gene 166:65-71(1995).
RN [2]
RP SEQUENCE OF 29-44.
RC STRAIN=IGC4052B;
RX MEDLINE=96132108; PubMed=8593683;
RA Steyn A.J.C., Pretorius I.S.;
RT "Characterization of a novel alpha-amylase from Lipomyces kononenkoae
RT and expression of its gene (LKAl) in Saccharomycetes cerevisiae.";
RL Curr. Genet. 28:526-533(1995).
CC -! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -! COPACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
CC at high concentrations (By similarity).
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC -! SIMILARITY: Contains 1 carbohydrate binding type-21 (CBM21)
CC domain.
-----
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-----
DR EMBL; U30376; AAC49622.1; ALT_INIT.
DR FIR; JC4510; JC4510.
DR HSSP; P10529; 7TAA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR005036; CBM_21.
DR Pfam; PF00128; Alpha-amylase; 1.
DR SMART; SM00642; Aamy; 1.
DR Pfam; PF03370; CBM_21; 1.
KW Glycoprotein; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 28
FT CHAIN 29 624 Alpha-amylase 1.
FT DOMAIN 40 133 Carbohydrate binding type-21.
FT ACT_SITE 353 353 Nucleophile (By similarity).
FT ACT_SITE 377 377 Proton donor (By similarity).
FT ACT_SITE 444 444 By similarity.
FT METAL 268 268 Calcium 1 (By similarity).
FT METAL 309 309 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 322 322 Calcium 1 (By similarity).
FT METAL 353 353 Calcium 2 (By similarity).
FT METAL 357 357 Calcium 1 (via carbonyl oxygen) (By
FT similarity).
FT METAL 377 377 Calcium 2 (By similarity).
FT DISULFID 177 185 By similarity.
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FT DISULFID 297 311 By similarity.
FT DISULFID 387 430 By similarity.
FT DISULFID 587 622 By similarity.
FT CARBOHYD 304 304 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 344 344 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 624 AA; 68876 MW; 87EB16534F5A9A9F CRC64;

Query Match 3.2%; Score 16; DB 1; Length 624;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 NYSIDGLRIDTVKHVQ 232
Db 344 NYSIDGLRIDTVKHVQ 359

RESULT 15
Q6YF33 PRELIMINARY; PRT; 647 AA.
AC Q6YF33;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Alpha-amylase.
OS Lipomyces starkeyi.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Lipomycetaceae; Lipomyces.
OX NCBI_TaxID=29829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM 22M;
RX PubMed=15043869; DOI=10.1016/j.femsle.2004.01.036;
RA Kang H.K., Lee J.H., Kim D., Day D.F., Robyt J.F., Park K.-H.,
RA Moon T.-W.;
RT "Cloning and expression of Lipomyces starkeyi alpha-amylase in
RT Escherichia coli and determination of some of its properties.";
RL FEMS Microbiol. Lett. 233:53-64(2004).
DR EMBL; AY155463; AAN75021.1; -.
DR HSSP; P26827; 1A47.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR005036; CBM_21.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF03370; CBM_21; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 647 AA; 70957 MW; D946071DB7560144 CRC64;

Query Match 3.2%; Score 16; DB 2; Length 647;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 217 NYSIDGLRIDTVKHVQ 232
Db 367 NYSIDGLRIDTVKHVQ 382
```

Search completed: November 7, 2005, 19:32:38
Job time : 266.382 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:58:55 ; Search time 286.494 Seconds
(without alignments)
672.288 Million cell updates/sec

Title: US-10-820-200-2
Perfect score: 498
Sequence: 1 MVAWSLFLYGLQVAPALA.....LPRVLPTKLAGSKICSSS 498

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	100.0	498	AAB84206	Aab84206 Amino aci
2	391	78.5	478	AAR72450	Aar72450 Aspergill
3	391	78.5	478	AAR78270	Aar78270 Aspergill
4	391	78.5	478	AAW14500	Aaw14500 Aspergill
5	384	77.1	498	ADT89632	Adt89632 Aspergill
6	384	77.1	499	ADT89628	Adt89628 Aspergill
7	377	75.7	1095	ABP96630	Abp96630 Alpha-amy
8	238	47.8	478	AAR79025	Aar79025 Mature ta
9	226	45.4	478	AAR46065	Aar46065 Mutant al
10	73	14.7	423	ABBO9072	Abbo9072 Aspergill
11	45	9.0	46	AAP70311	Aap70311 Sequence
12	45	9.0	46	AAP94631	Aap94631 Aspergill
13	45	9.0	46	AAR24437	Aar24437 Sequence
14	23	4.6	495	ABB80177	Abb80177 A. fumiga
15	20	4.0	20	ADP19639	Adp19639 Aspergill
16	20	4.0	21	ADM36200	Adm36200 Alpha-amy
17	20	4.0	21	ADO27369	Ado27369 A. niger
18	20	4.0	494	ABP97894	Abp97894 Amino aci
19	19	3.8	511	AAP81161	Aap81161 Recombina
20	19	3.8	511	AAPE1180	Aape1180 Sequence
21	19	3.8	512	AAR07574	Aar07574 Alpha-amy
22	19	3.8	513	ADN19570	Adn19570 Bacterial
23	18	3.6	46	AAP95651	Aap95651 N-termina
24	18	3.6	52	ADC22919	Adc22919 Conserved
25	18	3.6	54	AAP94633	Aap94633 N-termina

26	18	3.6	304	2	AAW44272	Aaw44272 Hybrid DN
27	18	3.6	306	2	AAW44269	Aaw44269 Hybrid DN
28	18	3.6	306	2	AAW44270	Aaw44270 Hybrid DN
29	18	3.6	307	2	AAW44273	Aaw44273 Hybrid DN
30	18	3.6	308	2	AAW44271	Aaw44271 Hybrid DN
31	18	3.6	630	6	ABB80178	Abb80178 A. fumiga
32	14	2.8	55	2	AAR88213	Aar88213 Alpha-amy
33	14	2.8	493	2	AAR88212	Aar88212 Alpha-amy
34	13	2.6	13	3	AAB12599	Aab12599 Amino aci
35	13	2.6	567	6	ABP97899	Abp97899 Amino aci
36	12	2.4	500	8	ADS23436	Ads23436 Bacterial
37	12	2.4	547	6	ABB80179	Abb80179 A. fumiga
38	12	2.4	549	6	ABP97895	Abp97895 Amino aci
39	12	2.4	555	6	ABP97896	Abp97896 Amino aci
40	11	2.2	49	1	AAP94634	Aap94634 N-termina
41	11	2.2	452	2	AAR63186	Aar63186 Variant a
42	11	2.2	468	2	AAR24136	Aar24136 Alpha-amy
43	11	2.2	468	2	AAR63184	Aar63184 Variant a
44	11	2.2	468	2	AAR63185	Aar63185 Variant a
45	11	2.2	468	2	AAR63187	Aar63187 Variant a

ALIGNMENTS

RESULT 1
AAB84206
ID AAB84206 standard; protein; 498 AA.
XX
AC AAB84206;
XX
DT 06-AUG-2001 (first entry)
XX
DE Amino acid sequence of a fungamyl-like alpha-amyase.
XX
KW Fungamyl-like alpha-amyase; glucoamylase; dextrinisation; maltose;
KW alcohol; starch; dough improver; brewing; starch liquification.
XX
OS Aspergillus oryzae.
XX
PN WO200134784-A1.
XX
PD 17-MAY-2001.
XX
PF 10-NOV-2000; 2000WO-DK000626.
XX
PR 10-NOV-1999; 99DK-00001617.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Bisgard-Frantzen H, Svendsen A, Pedersen S;
XX
DR WPI; 2001-367478/38.
XX
N-PSDB; AAP90208.
XX
PT New variant of Fungamyl-like alpha-amyase, useful for production of
PT maltose syrups, includes mutations that improve stability against heat
PT and acidic pH.
XX
PS Claim 1; Page 42-45; 49pp; English.
XX
CC The present sequence represents a fungamyl-like alpha-amyase. The
CC specification describes variants of this fungamyl-like alpha-amyase,
CC which have an alteration in one the amino acid regions 98-110, 150-160,
CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
CC substitution of an amino acid or an insertion of an amino acid downstream
CC of a particular position. The variants retain alpha-amyase activity, and
CC have better heat stability and/or stability at acidic pH, relative to
CC wild-type enzyme. The variants can therefore be used at higher
CC temperatures (more efficient conversion or faster reaction, and have
CC reduced need for cooling and reduced risk of contamination). The variants
CC may also be used in conjunction with other enzymes, particularly
CC glucoamylase during dextrinisation. The variants are used to produce

FT replaced with a fragment corresponding to 102-199 of
FT AAW14499, claim 42"
FT Misc-difference 165..117
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 195-202 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 21"
FT Misc-difference 166..117
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 196-198 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 23"
FT Misc-difference 181..184
FT /note= "an amino acid fragment corresponding to this
FT region is deleted from the parent sequence of a variant
FT Fungamyl; claim 43"
FT Misc-difference 291..313
FT /label= loop 8 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 322-346 of AAW14498 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 36"
FT Misc-difference 297..313
FT /label= loop 8 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 325-345 of AAW14498 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 38"
FT XX
PN WO9623874-A1.
XX
XX 08-AUG-1996.
XX PD
XX 05-FEB-1996; 96WO-DK000057.
XX PF
XX 03-FEB-1995; 95DK-00000128.
XX PR
XX 23-OCT-1995; 95DK-00001192.
XX PR
XX 10-NOV-1995; 95DK-00001256.
XX XX
XX (NOVO) NOVO-NORDISK AS.
XX PA
XX Svendsen A, Bisgard-Frantzen H, Borchert TV;
XX PI
XX WPI; 1996-371424/37.
XX DR
XX Alpha-amylase variants and methods of production - have altered
XX properties such as calcium dependency, substrate binding and stability.
XX Disclosure; Page 87-88; 171pp; English.
XX The present sequence is the mature Aspergillus oryzae alpha-amylase (A).
XX CC Variants of parent termamyl- and fungamyl-like alpha-amylases (and
XX methods of constructing them) are claimed. Examples of variants are
XX CC featured above. The variants have altered properties such as calcium
XX CC dependency, substrate binding and stability. Also one or more proline or
XX CC cysteine residues in the variant is modified or replaced with a non-
XX CC proline or non-cysteine residue such as alanine. The variants can be used
XX CC for (dish)washing, as detergent additives or for fabric desizing or
XX CC starch liquefaction. They can also be used for the production of
XX CC sweeteners and ethanol from starch. See also AAW14498-99
XX Sequence 478 AA;
XX Query Match 78.5%; Score 391; DB 2; Length 478;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 21 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYGCGTWQGIIDKLDYIQMGFTAI 80
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 ATPADWRSQSIYFLLTDRFARTDGTATCNTADQKYGCGTWQGIIDKLDYIQMGFTAI 60
Qy 81 WITPVTALPQTAYGDAYHGYWQDIYSLNENGTADDLKALSSALHERGMVMDVVA 140
Db 61 WITPVTALPQTAYGDAYHGYWQDIYSLNENGTADDLKALSSALHERGMVMDVVA 120
Qy 141 NHMGVDGAGSVDYSVFKPRSSQDYFHPFCFIQNYEDQTVEDCWLGDNVTVSLPDLDTTK 200
Db 121 NHMGVDGAGSVDYSVFKPRSSQDYFHPFCFIQNYEDQTVEDCWLGDNVTVSLPDLDTTK 180
Qy 201 DVVKNWYDMVGSLSVNSYIDGLRIDTVKHVQKDFWPGYNKAAGYVICGEVLGDPAYTC 260
Db 181 DVVKNWYDMVGSLSVNSYIDGLRIDTVKHVQKDFWPGYNKAAGYVICGEVLGDPAYTC 240
Qy 261 PYQNVMDGVLNYPPIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFVENHDNPR 320
Db 241 PYQNVMDGVLNYPPIYPLNNAFKSTSGMDDLNNMINTVKSDCPDSTLLGTFVENHDNPR 300
Qy 321 FASVTNDIALAKNVAAPFIILNDGPIIYVAGQEQHVAGGNDPANREATWLSGVPDTSLEYK 380
Db 301 FASVTNDIALAKNVAAPFIILNDGPIIYVAGQEQHVAGGNDPANREATWLSGVPDTSLEYK 360
Qy 381 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 411
Db 361 LIASANAIRNVAISKDTGFVTYKNWPIYKDD 391
RESULT 5
ID ADT89632
XX ADT89632 standard; protein; 498 AA.
AC ADT89632;
XX 16-DEC-2004 (first entry)
DT Aspergillus niger neutral alpha-amylase A (amyA) protein.
DE Glucoamylase; glaa; amyA; alpha-amylase A; enzyme.
XX Aspergillus niger.
OS US2004191864-A1.
XX PN 30-SEP-2004.
XX PD 31-MAR-2004; 2004US-00815495.
XX PF 31-MAR-2003; 2003US-0459902P.
XX PR (NOVO) NOVOZYMES BIOTECH INC.
XX PA Connelly M, Brody H;
XX PI WPI; 2004-708545/69.
XX DR N-PSDB; ADT89631.
XX XX Producing heterologous biological substance comprises culturing mutant of
XX wild-type Aspergillus niger strain in medium suitable for producing
XX heterologous biological substance and recovering heterologous biological
XX substance.
XX Example 11; SEQ ID NO 22; 58pp; English.
XX The present invention relates to a method of producing heterologous
XX biological substance. The method involves culturing mutant of wild-type
XX Aspergillus niger strain in medium suitable for producing heterologous
XX biological substance, where mutant strain comprises first nucleotide
XX sequence encoding heterologous biological substance and second nucleotide
XX sequences comprising modification of glucoamylase (glaA) and recovering
XX heterologous biological substance. the present sequence is the
XX Aspergillus niger neutral alpha-amylase A (amyA) protein.
XX Sequence 498 AA;

Query Match 77.1%; Score 384; DB 8; Length 498;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAWNSFLYGLQVAAPALAAPADWRSOSIYFLLTDRFARTDGGSTTATCNTADQKYCGG 60
DB 2 MYAWNSFLYGLQVAAPALAAPADWRSOSIYFLLTDRFARTDGGSTTATCNTADQKYCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMVLMVDVYVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQY 180
DB 122 KALSSALHERGMVLMVDVYVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQY 181

QY 181 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241

QY 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVNLPIYYPPLNNAFKSTSGSMDDLYNMINTVK 300
DB 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVNLPIYYPPLNNAFKSTSGSMDDLYNMINTVK 301

QY 301 SDCPDSTLLGTFVENHNDNPRFASYNNDIALAKNVAFAFIILNDGIPPIYAGQBQHYAGND 360
DB 302 SDCPDSTLLGTFVENHNDNPRFASYNNDIALAKNVAFAFIILNDGIPPIYAGQBQHYAGND 361

QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 6
ADT89628
ID ADT89628 standard; protein; 499 AA.

AC ADT89628;
XX
DT 16-DEC-2004 (first entry)
XX
DE Aspergillus niger neutral alpha-amylase B (amyB) protein.
XX
KW Glucoamylase; glaB; amyB; alpha-amylase B; enzyme.
XX
OS Aspergillus niger.
XX
PN US2004191864-A1.
XX
PD 30-SEP-2004.
XX
PF 31-MAR-2004; 2004US-00815495.
XX
PR 31-MAR-2003; 2003US-0459902P.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
XX
PI Connelly M, Brody H;
XX
DR WPI; 2004-708545/69.
DR N-PSDB; ADT89627.
XX
PT Producing heterologous biological substance comprises culturing mutant of
PT wild-type Aspergillus niger strain in medium suitable for producing
PT heterologous biological substance and recovering heterologous biological
PT substance.
XX
XX Example 10; SEQ ID NO 18; 58pp; English.
PS
XX
CC The present invention relates to a method of producing heterologous
CC biological substance. The method involves culturing mutant of wild-type
CC Aspergillus niger strain in medium suitable for producing heterologous

CC biological substance, where mutant strain comprises first nucleotide
CC sequence encoding heterologous biological substance and second nucleotide
CC sequences comprising modification of glucoamylase (glaA) and recovering .
CC heterologous biological substance. The present sequence is the
CC Aspergillus niger neutral alpha-amylase B (amyB) protein.

XX Sequence 499 AA;

Query Match 77.1%; Score 384; DB 8; Length 499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAWNSFLYGLQVAAPALAAPADWRSOSIYFLLTDRFARTDGGSTTATCNTADQKYCGG 60
DB 2 MYAWNSFLYGLQVAAPALAAPADWRSOSIYFLLTDRFARTDGGSTTATCNTADQKYCGG 61

QY 61 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 120
DB 62 TWQGIIDKLDYIQGMGFTAIWITPVTQAQLPQTAYGDAYHGYWQDDIYSLNENYGTADDL 121

QY 121 KALSSALHERGMVLMVDVYVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQY 180
DB 122 KALSSALHERGMVLMVDVYVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQY 181

QY 181 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 240
DB 182 VEDCWLGDNVTSLPDLDTTKDVVKNEWYDWVGSLSVNSYIDGLRIDTVKHVKQDFWPGYN 241

QY 241 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVNLPIYYPPLNNAFKSTSGSMDDLYNMINTVK 300
DB 242 KAAGVYCIGEVLDGDPAYTCPYQNVMDGVNLPIYYPPLNNAFKSTSGSMDDLYNMINTVK 301

QY 301 SDCPDSTLLGTFVENHNDNPRFASYNNDIALAKNVAFAFIILNDGIPPIYAGQBQHYAGND 360
DB 302 SDCPDSTLLGTFVENHNDNPRFASYNNDIALAKNVAFAFIILNDGIPPIYAGQBQHYAGND 361

QY 361 PANREATWLSGYPTDSELYKLIAS 384
DB 362 PANREATWLSGYPTDSELYKLIAS 385

RESULT 7

ADP96630
ID ADP96630 standard; protein; 1095 AA.

AC ADP96630;

XX
DT 02-JUN-2003 (first entry)

DE Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.

XX Self-processing plant; plant; processing enzyme; alpha-amylase; grain;
KW pullulanase; alpha-glucosidase; Glucose isomerase; glucoamylase;
KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW maltodextrin; ethanol; fermentation; beverage; enzyme.

XX Aspergillus shiroyami.
OS Synthetic.

XX WO2003018766-A2.

XX PD 06-MAR-2003.

XX PF 27-AUG-2002; 2002WO-US0271129.

XX PR 27-AUG-2001; 2001US-0315281P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Lanahan MB, Basu SS, Battie CJ, Chen W, Craig J, Kinkema M;

XX WPI; 2003-268420/26.

DR N-PSDB; ACC44572.

XX Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
 PT alpha-amylase, useful for producing plant to produce food products having
 PT improved taste or fermentable substrates for ethanol.
 XX
 PS Claim 1; Page 107; 158pp; English.
 XX
 CC The present invention describes polynucleotides which encode processing
 CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
 CC isomerase, or glucoamylase) that are optimised for expression in plants.
 CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
 CC processing enzymes, which are activated under suitable conditions to act
 CC upon the desired substrate. Also described are self-processing transgenic
 CC plants and plant parts, e.g. grain, which express one or more of these
 CC enzymes and have an altered composition that facilitates plant and grain
 CC processing. Also described is a method (M) for converting starch to
 CC starch-derived products in a transformed plant part (TPP), by activating
 CC the starch processing enzyme contained in it. Transgenic grain is useful
 CC for preparing maltodextrin. A transformed plant (TP) can be used to
 CC produce food products having improved taste and to produce fermentable
 CC substrates for ethanol and fermented beverages. (M) eliminates the need
 CC to mill or physically disrupt the integrity of plant parts prior to
 CC recovery of starch-derived products. The present sequence represents
 CC alpha-amylase/glucoamylase fusion protein, which is given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1095 AA;

Query Match 75.7%; Score 377; DB 6; Length 1095;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 477; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 21 ATPDWRSSISYFLTDRPARTDGGTTATCNADQKCGGTWQGIIDKLDYIQNGFTAI 80
 DB 1 ATPDWRSSISYFLTDRPARTDGGTTATCNADQKCGGTWQGIIDKLDYIQNGFTAI 60
 QY 81 WITPVTALPQTAYGDAYHGYYQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 140
 DB 61 WITPVTALPQTAYGDAYHGYYQDDIYSLNENYGTADDLKALSSALHERGMYLMDVVA 120
 QY 141 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTVEDCWLGDNTVSLPDLDTTK 200
 DB 121 NHMGYDAGSSVDYSVFKPFSSQDYFHPFCFTQNYEDQTVEDCWLGDNTVSLPDLDTTK 180
 QY 201 DVVKNEWYDWSLSVNSYIDGLRDTVKHVKQDFWPGYNKAAGYVCIGEVLDGDPATC 260
 DB 181 DVVKNEWYDWSLSVNSYIDGLRDTVKHVKQDFWPGYNKAAGYVCIGEVLDGDPATC 240
 QY 261 PYQNYMDGVLNPIIYYPPLNFAFKSTSGSMDLLYNMINTVKSDCPDSTLLGTFVENHDNPR 320
 DB 241 PYQNYMDGVLNPIIYYPPLNFAFKSTSGSMDLLYNMINTVKSDCPDSTLLGTFVENHDNPR 300
 QY 321 FASYTNDIALAKNVAAPFIILNDGIPIIYAGQEQHYAGNDPANREATWLSGYPTDSLYK 380
 DB 301 FASYTNDIALAKNVAAPFIILNDGIPIIYAGQEQHYAGNDPANREATWLSGYPTDSLYK 360
 QY 381 LIASANALRNVAISKDTGPTVTKNMPYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 440
 DB 361 LIASANALRNVAISKDTGPTVTKNMPYKDDTTIAMRKGTGDSQIVTILSNKGASGDSVT 420
 QY 441 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVFPVMAGGLPRVLYPTEKLAGSKICSSS 498
 DB 421 LSLSGAGYTAGQQLTEVIGCTTIVTSGDGNVFPVMAGGLPRVLYPTEKLAGSKICSSS 478

RESULT 8
 AAR79025
 ID AAR79025 standard; protein; 478 AA.
 XX
 AC AAR79025;
 XX
 DT 22-MAR-1996 (first entry)
 XX

DE Mature taka-amylase A.
 XX
 KW Wild type; neopullulanase; B. stearothermophilus; mutant; food industry;
 KW modification; hydrophobicity; replacement insertion; deletion.
 XX
 OS Aspergillus oryzae.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 30..38
 FT Disulfide-bond 150..164
 FT Disulfide-bond 240..283
 FT Disulfide-bond 439..474
 XX
 PN JP07177891-A.
 XX
 PD 18-JUL-1995.
 XX
 PF 31-OCT-1994; 94JP-00288658.
 XX
 PR 12-NOV-1993; 93JP-00306096.
 XX
 PA (NIDE) NEC CORP.
 PA (EZAK) EZAKI GLICO CO.
 XX
 DR WPI; 1995-279919/37.
 XX
 PT Modifying a transferase by enhancing hydrophobicity of a selected site -
 PT increases transfer activity, also new mutant neo-pullulanase (S).
 XX
 PS Disclosure; Page 10-11; 18pp; English.
 XX
 CC This sequence represents the mature form of taka-amylase from A. oryzae.
 CC This sequence was used in a method for the generation of mutant
 CC pullulanases for use in the food industry (see also AAR79028-28). The
 CC wild type pullulanase enzyme was modified by the method of the invention
 CC for enhancing the hydrophobicity of a selected site of the pullulanase.
 CC The method comprises replacement of a group in the selected site with a
 CC hydrophobic group, replacement of an amino acid with a hydrophobic amino
 CC acid, and/or insertion or deletion of a hydrophobic amino acid from the
 CC selected site. The method was used to produce neopullulanases Y377F,
 CC S422V and M375L
 XX
 SQ Sequence 478 AA;
 Query Match 47.8%; Score 238; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 8.5e-219;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 106 DIYSINENYGTADDLKALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDY 165
 DB 86 DIYSINENYGTADDLKALSSALHERGMYLMDVVDVANHMGYDAGSSVDYSVFKPFSSQDY 145
 QY 166 FHPFCFTQNYEDQTVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWSLSVNSYIDGLRI 225
 DB 146 FHPFCFTQNYEDQTVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWSLSVNSYIDGLRI 205
 QY 226 DTVKHVKQDFWPGYNKAAGYVCIGEVLDGDPATCPCYQNYMDGVLNPIIYYPPLNFAFKST 285
 DB 206 DTVKHVKQDFWPGYNKAAGYVCIGEVLDGDPATCPCYQNYMDGVLNPIIYYPPLNFAFKST 265
 QY 286 SGSMDLLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAPFIILNDG 343
 DB 266 SGSMDLLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAPFIILNDG 323
 RESULT 9
 AAR46065
 ID AAR46065 standard; protein; 478 AA.
 XX
 AC AAR46065;
 XX
 DT 25-MAR-2003 (revised)
 DT 18-JUL-1994 (first entry)
 XX

XX DE Mutant alpha-amylase.
 XX KW Methionine substitution; stability; activity; detergent;
 XX KW dishwashing agents; liquefaction agents.
 XX OS Aspergillus oryzae.
 XX WO9402597-A1.
 XX PD 03-FEB-1994.
 XX PF 06-JUL-1993; 93WO-DK000230.
 XX PR 23-JUL-1992; 92DK-00000946.
 XX PR 16-DEC-1992; 92DK-00001503.
 XX PR 15-MAR-1993; 93DK-00000292.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Biegard-Prantzen H;
 XX WPI; 1994-048855/06.
 XX PT Mutant alpha-amylase from Bacillus species comprising a methionine
 PT substitution - with improved stability and activity at low pH, for use in
 PT detergents, dishwashing agents and liquefaction agents.
 XX PS Claim 1; Page 7; 20pp; English.
 XX CC The sequence as that of the Aspergillus oryzae alpha amylase, sold
 CC commercially as FUNGAMYL (TM) by Novo Nordisk A/S. The sequence can be
 CC mutated by substitution of one or more of its methionine residues for any
 CC amino acid other than cysteine. The mutant alpha-amylase exhibits a
 CC better activity level and better stability in the presence of oxidising
 CC agents than previous mutant alpha amylases, and improved thermostability
 CC at moderately low pH. The enzyme can be used as an additive for
 CC detergents, dishwashing agents and liquefaction agents. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX SQ Sequence 478 AA;
 Query Match 45.4%; Score 226; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 2.7e-207;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 186 LGDNTVSLPDLDTTKDVVKNWYDWVGSLSVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGV 245
 DB 166 LGDNTVSLPDLDTTKDVVKNWYDWVGSLSVSNYSIDGLRIDTVKHVKQDFWPGYNKAAGV 225
 QY 246 YCIGEVLDGDPATCPYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLNNMINTVKSDCPD 305
 DB 226 YCIGEVLDGDPATCPYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLNNMINTVKSDCPD 285
 QY 306 STLLGTFVFNHNDNPRFASVTNDIALAKNVAAFIILNDGPIIYVAGQEQHYAGNDPANRE 365
 DB 286 STLLGTFVFNHNDNPRFASVTNDIALAKNVAAFIILNDGPIIYVAGQEQHYAGNDPANRE 345
 QY 366 ATWLSGYPTDSELYKLIASNAIRNVAISKDTGFTYKNWPIYKDD 411
 DB 346 ATWLSGYPTDSELYKLIASNAIRNVAISKDTGFTYKNWPIYKDD 391
 RESULT 10
 ABB09072
 ID ABB09072 standard; protein; 423 AA.
 XX AC ABB09072;
 XX DT 26-JUN-2002 (first entry)
 XX DE Aspergillus oryzae TAKA protein (TAA).
 XX

KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
 KW protein co-ordinate data; 3 dimensional structure.
 XX OS Aspergillus oryzae.
 XX KR2001027418-A.
 XX PD 06-APR-2001.
 XX PF 09-SEP-1999; 99KR-00039130.
 XX PR 09-SEP-1999; 99KR-00039130.
 XX PA (POST-) POSTECH FOUND.
 XX PA (SAMY-) SAMYANG GENEX CORP.
 XX PI Kim TJ, Park GH;
 XX DR WPI; 2001-534477/59.
 XX PT Manufacturing maltogenic amylase having improved transglycosylation
 PT activity, comprises using crystallization.
 XX PS Disclosure; Page 188; 196pp; Korean.
 XX CC The present invention describes manufacturing maltogenic amylase (EC
 CC 3.2.1.133) having improved transglycosylation activity, comprising using
 CC crystallisation and the three dimensional structure of maltogenic
 CC amylase. Manufacturing maltogenic amylase comprises the following steps:
 CC (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC
 CC 5027BP) and inserting the gene into plasmid pUC119 to construct
 CC recombinant DNA (pTHW119); (ii) inserting the recombinant DNA to
 CC Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius
 CC for 10 hours in Luria-Bertani (LB) media and centrifuging the media to
 CC obtain a microbial cell; (iii) suspending the microbial cell with buffer
 CC solution at pH 7.5 and obtaining supernatant; and (iv) passing the
 CC supernatant through column chromatography and obtaining purified
 CC maltogenic amylase. The maltogenic amylase is a dimer comprised of two
 CC maltogenic amylase molecules, and a Thermus sp. IM6501 maltogenic amylase
 CC (ThMA) crystal. The amylase has a structure containing an activated
 CC region that consists of amino acid residues of Asp-328, Glu-357, Asp-424,
 CC and a pocket with glucose bound that consists of amino acid residues of
 CC Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn131, Glu132, Val1329,
 CC and His1360. The present sequence represents Aspergillus oryzae TAKA
 CC protein (TAA), given in comparison with ThMA in the present invention
 XX SQ Sequence 423 AA;
 Query Match 14.7%; Score 73; DB 4; Length 423;
 Best Local Similarity 100.0%; Pred. No. 8.9e-61;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 248 IGEVLGDGPATCPYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLNNMINTVKSDCPDST 307
 DB 224 IGEVLGDGPATCPYQNVMDGVLNPIYYPILLNAFKSTSGSMDDLNNMINTVKSDCPDST 283
 QY 308 LLGTFVFNHNDNPR 320
 DB 284 LLGTFVFNHNDNPR 296
 RESULT 11
 AAP70311
 ID AAP70311 standard; protein; 46 AA.
 XX AC AAP70311;
 XX DT 24-OCT-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 18-FEB-1991 (first entry)
 XX DE Sequence encoded by the prerregion and the 5' part of the structural gene
 DE for the TAKA-amylase.

```

XX Aspergillus gene expression.
KW Aspergillus oryzae; Hw325.
XX
OS Aspergillus oryzae; Hw325.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT Protein 22..46
XX
XX EP238023-A.
XX
XX 23-SEP-1987.
XX
XX 16-MAR-1987; 87EP-00103806.
XX
XX 17-MAR-1986; 86DK-00001226.
XX
XX 17-MAR-1987; 87DK-00001353.
XX
XX (NOVO ) NOVO TERAPEUTISK LAB AS.
XX
XX Boel E, Christensen T, Woeldike HF;
XX
XX WPI; 1987-265414/38.
XX
XX N-PSDB; AAN70507.
XX
XX Expressing proteins, esp. enzymes, in Aspergillus oryzae - by
XX PT transforming with recombinant vector, pref. contg. the TAKA amylase
XX PT promoter system.
XX
XX Disclosure; Fig 1; 39pp; English.
XX
XX The patent claims a process for the production of protein products in
XX CC Aspergillus oryzae and a promoter for use in Aspergillus. The process
XX CC enables industrial production of many different polypeptides and proteins
XX CC in A. oryzae. Examples of such products are chymosin or prochymosin and
XX CC other rennets, proteases, lipases and amylases. (Updated on 25-MAR-2003
XX CC to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX CC (Updated on 24-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 46 AA;
XX
Query Match 9.0%; Score 45; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 7.1e-35;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAWNSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGS 45
DB 2 MVAWNSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGS 46
XX
RESULT 12
AAP94631
ID AAP94631 standard; protein; 46 AA.
XX
XX AAP94631;
XX
XX 25-MAR-2003 (revised)
XX 01-JUL-1990 (first entry)
XX
XX Aspergillus niger neutral alpha-amylase including prerregion as encoded by
XX DE plasmids pNA1 and pNA2.
XX
XX Aspergillus niger DSM 2761; neutral alpha-amylase; presequence;
XX KW plasmid pNA1; plasmid pNA2.
XX
XX Aspergillus niger.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT Protein /note= "Prerregion"
XX 22..46
XX /note= "N-terminal portion"
XX

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PN W08901969-A.
XX
XX 09-MAR-1989.
XX
XX 02-SEP-1988; 88WO-DK000145.
XX
XX 04-SEP-1987; 87DK-00004609.
XX 29-SEP-1987; 87DK-00005126.
XX
XX (NOVO ) NOVO IND AS.
XX
XX Woeldike H;
XX
XX WPI; 1989-085543/11.
XX
XX N-PSDB; AAN91273, AAN91274.
XX
XX Prodn. of proteins in Aspergillus - using promoter and upstream
XX PT activating sequences derived from Aspergillus niger amylase genes.
XX
XX Fig 2; page 2/11; 38pp; English.
XX
XX The DNA was prepared from mycelium from A. niger DSM 2761. It was
XX CC screened with a hybridisation probe from TAKA-amylase cDNA and two
XX CC hybridising clones were found. Plasmids pNA1 and pNA2 each carry the full
XX CC length amylase gene with promoters and upstream activating sequences.
XX CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
XX CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX SQ Sequence 46 AA;
XX
Query Match 9.0%; Score 45; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 7.1e-35;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAWNSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGS 45
DB 2 MVAWNSFLYGLQVAAPALAAATPADWRSQSIYFLLTDRFARTDGS 46
XX
RESULT 13
AAR24437
ID AAR24437 standard; protein; 46 AA.
XX
XX AAR24437;
XX
XX 24-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 21-NOV-1992 (first entry)
XX
XX Sequence of TAKA-amylase signal and mature protein.
XX
XX Yeast promoter; expression vector; TAKA-amylase; alpha-amylase.
XX
XX Aspergillus oryzae; Hw325.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT /label= signal
XX
XX EP489718-A1.
XX
XX 10-JUN-1992.
XX
XX 16-MAR-1987; 92EP-00104421.
XX
XX 17-MAR-1986; 86DK-00001226.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Boel E, Christensen T, Woeldike HF;
XX
XX WPI; 1992-193872/24.
XX
XX N-PSDB; AAQ24569.
XX

```

XX Promoter providing efficient protein prodn. in Aspergillus - is the TAKA
PT amylase promoter, opt. with activating sequences, giving high yields of
PT homologous or heterologous enzymes.
XX Disclosure; Fig 1; 41pp; English.
XX The DNA whose sequence is in AQ024569 was derived from the TAKA- amylase
CC clone. It was inserted in BamHI digested pBR322 to give plasmid pTAKA 17.
CC In pTAKA 17 the A. oryzae derived DNA is shown as a 5.5 kb BamHI/Sau 3AI
CC - BamHI/Sau 3AI fragment, the promoter and upstream activating sequences
CC representing a 2.1 kb fragment. In the method according to the present
CC invention the sequence from nucleotide -1144 to nucleotide -10 has been
CC used as one example of a well functioning part of the promoter region. In
CC another embodiment of the present invention the nucleotide sequence from
CC nucleotide - 1176 to -1 was preceded by the still not sequenced 1.05 kb
CC fragment from pTAKA 17. (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to
CC correct PF field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX Sequence 46 AA;
XX
XX Query Match 9.0%; Score 45; DB 2; Length 46;
XX Best Local Similarity 100.0%; Pred. No. 7.1e-35;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLTLTDRPARTDGS 45
DB 2 MVAMWSFLYGLQVAAPALAAATPADWRSQSIYFLTLTDRPARTDGS 46
XX
XX RESULT 14
XX ABB80177
XX ID ABB80177 standard; protein; 495 AA.
XX AC ABB80177;
XX
XX 11-AUG-2003 (first entry)
XX
XX A. fumigatus AfaAL1.
XX Enzyme; tannase; cellulase; glucose oxidase; glucoamylase; phytase;
KW beta-galactosidase; invertase; lipase; alpha-amylase; laccase;
KW polygalacturonase; xylanase; gallate ester linkage; detergent; cellulose;
KW glucose; oxygen; myo-inositol phosphate; lactose; tea leaf; sucrose;
KW glyceride; starch; maltodextrin; oxidated phenolic compound;
KW polygalacturonic acid chain; xylan; xylo-oligomer; food; feed; beverage;
KW textile; tea liquor; cleaning ability.
XX
XX Aspergillus fumigatus.
XX
XX WO2003012071-A2.
XX
XX 13-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024842.
XX
XX 03-AUG-2001; 2001US-0309870P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Jiang B, Storms R, Roemer T, Bussey H;
XX
XX WPI: 2003-332729/31.
XX N-PSDB; ABQ80345, ABQ80346.
XX
XX Novel isolated Aspergillus fumigatus polypeptide, useful in various
PT industries such as those involved in the making of food and feed,
PT beverages, textiles and detergents.
XX
XX Claim 17; Page 134-35; 169pp; English.
XX

CC The sequences given in ABB80164-87 show enzymatic proteins derived from
CC A. fumigatus. These proteins display the catalytic activity of an enzyme
CC such as tannase, cellulase, glucose oxidase, glucoamylase, phytase, beta-
CC galactosidase, invertase, lipase, alpha-amylase, laccase,
CC polygalacturonase or xylanase. Compositions comprising the tannase are
CC useful for modulating the amount of compounds that comprise a gallate
CC ester linkage in a composition. Compositions comprising cellulase are
CC useful for modulating the amount of cellulose in a composition.
CC Compositions comprising glucose oxidase are useful for modulating the
CC amount of glucose or oxygen in a composition. Compositions comprising
CC phytase are useful for modulating the amount of myo-inositol phosphates
CC in a composition. Compositions comprising beta-galactosidase are useful
CC for modulating the amount of lactose in a composition. Compositions
CC comprising sucrose or invertase are useful for modulating the amount of
CC sucrose in a composition. Compositions comprising lipase are useful for
CC modulating the amount of glyceride in a composition. Compositions
CC comprising alpha-amylases are useful for modulating the amount of
CC starches or maltodextrins in a composition. Compositions comprising
CC laccase are useful for modulating the amount of oxidated phenolic
CC compounds in a composition. Compositions comprising polygalacturonases
CC are useful for modulating the amount of high or low molecular weight
CC polygalacturonic acid chains in a composition. Compositions comprising
CC xylanases are useful for modulating the amount of xylan or xylo-oligomers
CC in a composition. The A. fumigatus proteins and corresponding DNA's are
CC useful in various industries such as those involved in the making of food
CC and feed, beverages, textiles and detergents. The DNA's are useful to
CC express recombinant enzymes for characterization, modification or
CC industrial uses, to compare with the nucleotide sequence of A. fumigatus
CC to identify duplicated genes of paralogs having the same or similar
CC biochemical activity and/or function, to compare with nucleic acid
CC sequence of other related or distant fungal organisms to identify
CC potential orthologous enzyme genes, for selecting and making oligomers
CC for attachment to a nucleic acid array for examination of expression
CC patterns, and to raise anti-protein antibodies. The polypeptide having
CC tannase activity increases the yield of tea liquor from tea leaves,
CC improves the colour, flavour and health benefits of tea products,
CC particularly an instant tea product. The polypeptide having cellulase
CC activity enhances cleaning ability of detergent compositions
XX
XX Sequence 495 AA;
XX

Query Match 4.6%; Score 23; DB 6; Length 495;
Best Local Similarity 100.0%; Pred. No. 8.2e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 WRSQSIYFLTLTDRPARTDGSITTA 48
DB 25 WRSQSIYFLTLTDRPARTDGSITTA 47
XX
XX RESULT 15
XX ADP19639
XX ID ADP19639 standard; peptide; 20 AA.
XX AC ADP19639;
XX
XX 09-SEP-2004 (first entry)
XX
XX Aspergillus oryzae fungamyl signal peptide sequence.
XX filamentous fungus; signal peptide; fungamyl.
XX Aspergillus oryzae.
XX WO2004050695-A2.
XX
XX 17-JUN-2004.
XX
XX 05-DEC-2003; 2003WO-DK000838.
XX
XX 05-DEC-2002; 2002DK-00001875.
XX
XX (NOVO) NOVOZYMES AS.

XX Hansen TM;
PI
XX
XX
DR WPI; 2004-450719/42.
XX
XX Producing a polypeptide of interest in a filamentous fungus comprises
PT providing a modified DNA sequence by inserting a DNA sequence encoding
PT one or more amino acid residues in between 2 DNA sequences.
XX
XX
PS Disclosure; SEQ ID NO 3; 36pp; English.
XX
XX The invention relates to a method of producing a polypeptide of interest
CC in a filamentous fungus comprising providing a modified DNA sequence by
CC inserting a DNA sequence encoding one or more amino acid residues in
CC between a DNA sequence encoding a polypeptide of interest and the
CC adjacent upstream DNA sequence encoding the N-terminal signal peptide.
CC The methods, DNA sequence, DNA construct and expression vector are useful
CC for producing a polypeptide of interest. This sequence corresponds to the
CC signal peptide sequence from the Aspergillus oryzae fungamyl protein used
CC for producing the polypeptide of interest by the method of the invention.
XX
SQ Sequence 20 AA;
Query Match 4.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAWWSFLYGLQVAAPALA 20
Db 1 MYAWWSFLYGLQVAAPALA 20

Search completed: November 7, 2005, 19:27:54
Job time : 288.494 secs

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OM protein - protein search, using sw model

Run on: November 7, 2005, 18:25:16 ; Search time 4.09459 Seconds
(without alignments)
661.194 Million cell updates/sec

Title: US-10-820-200-2_COPY_161_167

Perfect score: 40

Sequence: 1 SSQDYFH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003Bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	423	4	ABB09072 Aspergill
2	40	100.0	478	2	Aar46065 Mutant al
3	40	100.0	478	2	Aar72450 Aspergill
4	40	100.0	478	2	Aar78270 Aspergill
5	40	100.0	478	2	Aar79025 Mature ta
6	40	100.0	478	2	Aaw14500 Aspergill
7	40	100.0	498	4	Aab84206 Amino aci
8	40	100.0	498	8	Adt89632 Aspergill
9	40	100.0	499	8	Adt89628 Aspergill
10	40	100.0	1095	6	Abp96630 Alpha-amy
11	37	92.5	493	2	Aar88212 Alpha-amy
12	34	85.0	498	4	Aao08447 Human pol
13	34	85.0	1222	3	Aag36453 Arabidops
14	34	85.0	1257	3	Aag36452 Arabidops
15	34	85.0	1275	3	Aag36451 Arabidops
16	33	82.5	116	5	Abp08801 Human ORF
17	33	82.5	124	4	Aao05772 Human pol
18	33	82.5	342	6	Abu70873 Human adi
19	33	82.5	379	8	Ado58298 S. Gomunc
20	33	82.5	2112	7	Adg76988 Human nuc
21	33	82.5	3124	8	Adj78494 EIA bindi
22	33	82.5	4351	7	Adg42622 Rat MEGFI
23	32	80.0	82	8	Adn05042 Antipsori
24	32	80.0	82	8	Adp25302 PRO polyp
25	32	80.0	84	8	Adk47501 Streptoco

26	32	80.0	95	8	ADR95807	Adr95807 Novel S.
27	32	80.0	119	5	ABP42992	Abp42992 Human ova
28	32	80.0	180	6	ABU00681	Abu00681 S. pneumo
29	32	80.0	180	6	ADM92084	Adm92084 S. pneumo
30	32	80.0	182	5	ABP28341	Abp28341 Streptoco
31	32	80.0	195	8	ADH45430	Adh45430 Human mol
32	32	80.0	223	6	ABU44715	Abu44715 Protein e
33	32	80.0	326	6	ABP98616	Abp98616 Mature Er
34	32	80.0	348	6	ADP98615	Adp98615 Erwinia c
35	32	80.0	351	8	ADO61605	Ado61605 Transcrip
36	32	80.0	501	4	ABG15126	Abg15126 Novel hum
37	32	80.0	529	4	ABB70891	Abb70891 Drosophil
38	32	80.0	583	2	Aaw26654	Aaw26654 Human PAN
39	32	80.0	583	6	ABM72922	Abm72922 Novel hum
40	32	80.0	583	8	ABM81509	Abm81509 Tumour-as
41	32	80.0	583	8	ADP25358	Adp25358 PRO polyp
42	32	80.0	594	3	AAB56501	Aab56501 Human pro
43	32	80.0	685	7	ADK62434	Adk62434 Disease t
44	32	80.0	700	2	AAY33673	Aay33673 B. baasia
45	32	80.0	715	4	AAM79737	Aam79737 Human pro

ALIGNMENTS

RESULT 1
ABB09072
ID ABB09072 standard; protein; 423 AA.
XX
AC ABB09072;
XX
DT 26-JUN-2002 (first entry)
XX
DE Aspergillus oryzae TAKA protein (TAA).
XX
KW Thermus sp. IM6501; maltogenic amylase; EC 3.2.1.133; crystallisation;
KW protein co-ordinate data; 3 dimensional structure.
XX
OS Aspergillus oryzae.
XX
PN KR2001027418-A.
XX
PD 06-APR-2001.
XX
PF 09-SEP-1999; 99KR-00039130.
XX
PR 09-SEP-1999; 99KR-00039130.
XX
(POST-) POSTECH FOUND.
(SAMY-) SAMYANG GENEX CORP.
XX
Kim TJ, Park GH;
XX
WPI; 2001-534477/59.
XX
Manufacturing maltogenic amylase having improved transglycosylation activity, comprises using crystallization.
XX
Disclosure; Page 188; 196pp; Korean.

The present invention describes manufacturing maltogenic amylase (EC 3.2.1.133) having improved transglycosylation activity, comprising using crystallisation and the three dimensional structure of maltogenic amylase. Manufacturing maltogenic amylase comprises the following steps: (i) obtaining a gene of maltogenic amylase from Thermus sp. IM6501 (KCTC 5027BP) and inserting the gene into plasmid pUC19 to construct recombinant DNA (pRW119); (ii) inserting the recombinant DNA to Escherichia coli MC1061, which is cultivated at 37 plus degrees Celsius for 10 hours in Luria-Bertani (LB) media and centrifuging the media to obtain a microbial cell; (iii) suspending the microbial cell with buffer solution at pH 7.5 and obtaining supernatant; and (iv) passing the supernatant through column chromatography and obtaining purified maltogenic amylase. The maltogenic amylase is a dimer comprised of two

CC maltogenic amylase molecules, and a *Thermus* sp. IM6501 maltogenic amylase (ThMA) crystal. The amylase has a structure containing an activated region that consists of amino acid residues of Asp-328, Glu-357, Asp-424, and a pocket with glucose bound that consists of amino acid residues of Pro44, Tyr45, Arg81, Arg83, Pro118, Cys116, Asn1331, Glu1332, Val1329, CC and His1360. The present sequence represents *Aspergillus oryzae* TAKA CC protein (TAA), given in comparison with ThMA in the present invention XX
SQ Sequence 423 AA;

Query Match 100.0%; Score 40; DB 4; Length 423;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 137 SSQDYFH 143

RESULT 2
AAR46065
ID AAR46065 standard; protein; 478 AA.
XX
AC AAR46065;

DT 25-MAR-2003 (revised)
DT 18-JUL-1994 (first entry)

DE Mutant alpha-amylase.

KW Methionine substitution; stability; activity; detergent;
KW dishwashing agents; liquifaction agents.

OS *Aspergillus oryzae*.

PN WO9402597-A1.

PD 03-FEB-1994.

PF 06-JUL-1993; 93WO-DK000230.

PR 23-JUL-1992; 92DK-00000946.

PR 16-DEC-1992; 92DK-00001503.

PR 15-MAR-1993; 93DK-00000292.

PA (NOVO) NOVO-NORDISK AS.

PI Svendsen A, Bisgard-Frantzen H;

DR WPI; 1994-048855/06.

PT Mutant alpha-amylase from *Bacillus* species comprising a methionine substitution - with improved stability and activity at low pH, for use in PT detergents, dishwashing agents and liquifaction agents.

PS Claim 1; Page 7; 20pp; English.

XX The sequence as that of the *Aspergillus oryzae* alpha amylase, sold commercially as FUNGAWYL (TM) by Novo Nordisk A/S. The sequence can be mutated by substitution of one or more of its methionine residues for any amino acid other than cysteine. The mutant alpha-amylase exhibits a better activity level and better stability in the presence of oxidising agents than previous mutant alpha amylases, and improved thermostability at moderately low pH. The enzyme can be used as an additive for CC detergents, dishwashing agents and liquifaction agents. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 478 AA;

Query Match 100.0%; Score 40; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 3
AAR72450
ID AAR72450 standard; protein; 478 AA.

XX
AC AAR72450;

DT 25-MAR-2003 (revised)

DT 01-DEC-1995 (first entry)

DE *Aspergillus oryzae* alpha amylase (mature protein).

XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; *Bacillus licheniformis*; *Bacillus amyloliquefaciens*;
KW *Bacillus stearothermophilus*; dyeing; bleaching; scouring; textile;
KW thermostable.

OS *Aspergillus oryzae*.

PN WO9510603-A1.

PD 20-APR-1995.

PF 05-OCT-1994; 94WO-DK000370.

PR 08-OCT-1993; 93DK-00001133.

PR 02-FEB-1994; 94DK-00000140.

PA (NOVO) NOVO-NORDISK AS.

PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;

PI Van Der Zee P;

DR WPI; 1995-161790/21.

PT New *Bacillus* derived alpha-amylase variants - having amino acid PT modifications to improve washing and/or dishwashing performance.

XX Disclosure; Page 75-76; 105pp; English.

XX Variant alpha amylase enzymes which have improved washing and/or as CC detergent additives. The enzymes have one or more amino acid residues added, deleted or substituted. The variants can also be used for textile CC desizing prior to scouring, bleaching and dyeing. The variants have CC improved thermostability, acid/alkaline stability; low temperature CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 478 AA;

Query Match 100.0%; Score 40; DB 2; Length 478;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
Db 141 SSQDYFH 147

RESULT 4
AAR78270
ID AAR78270 standard; protein; 478 AA.

XX
AC AAR78270;

DT 17-JAN-1996 (first entry)

DE *Aspergillus oryzae* alpha amylase (mature protein).

FT to 12-19 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 30"
FT
FT Misc-difference 32.. 38
FT /label= loop 1 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 14-15 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 32"
FT
FT Misc-difference 66.. 84
FT /label= loop 2 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 44-57 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 18"
FT
FT Misc-difference 70.. 78
FT /label= loop 2 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 48-51 of AAW14499 is deleted
FT or replaced with a fragment corresponding to this
FT fragment; claim 20"
FT
FT Misc-difference 99.. 120
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 117-185 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 24"
FT
FT Misc-difference 102.. 1206
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 121-181 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 26"
FT
FT Misc-difference 121.. 181
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to this fragment is deleted or replaced with a fragment
FT corresponding to 102-206 of AAW14499; claim 41"
FT
FT Misc-difference 121.. 1174
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to this fragment is deleted or
FT replaced with a fragment corresponding to 102-199 of
FT AAW14499; claim 42"
FT
FT Misc-difference 165.. 1177
FT /label= loop 3 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 195-202 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 21"
FT
FT Misc-difference 166.. 1173
FT /label= loop 3 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for
FT a variant) corresponding to 196-198 of AAW14499 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 23"
FT
FT Misc-difference 181.. 1184
FT /note= "an amino acid fragment corresponding to this
FT region is deleted from the parent sequence of a variant
FT Fungamyl; claim 43"
FT
FT Misc-difference 291.. 1313
FT /label= loop 8 modification region
FT /note= "at least one amino acid residue of a parent alpha
FT -amylase (used as a template for a variant) corresponding
FT to 322-346 of AAW14499 is deleted or replaced with a
FT fragment corresponding to this fragment; claim 36"
FT
FT Misc-difference 297.. 1313
FT /label= loop 8 modification region
FT /note= "preferred region where at least one amino acid
FT residue of a parent alpha-amylase (used as a template for

FT a variant) corresponding to 325-345 of AAW14498 is
FT deleted or replaced with a fragment corresponding to this
FT fragment; claim 38"
FT
FT WO9623974-A1.
FT
FT 08-AUG-1996.
FT
FT 05-FEB-1996; 96WO-DK0000057.
FT
FT 03-FEB-1995; 95DK-00000128.
FT 23-OCT-1995; 95DK-00001192.
FT 10-NOV-1995; 95DK-00001256.
FT
FT (NOVO) NOVO-NORDISK AS.
FT
FT Svendsen A, Bisgard-Frantzen H, Borchert TV;
FT WPI; 1996-371424/37.
FT
FT Alpha-amylase variants and methods of production - have altered
FT properties such as calcium dependency, substrate binding and stability.
FT
FT Disclosure; Page 87-88; 171pp; English.
FT
FT The present sequence is the mature Aspergillus oryzae alpha-amylase (A).
FT Variants of parent termamyl- and fungamyl-like alpha-amylases (and
FT methods of constructing them) are claimed. Examples of variants are
FT featured above. The variants have altered properties such as calcium
FT dependency, substrate binding and stability. Also one or more proline or
FT cysteine residues in the variant is modified or replaced with a non-
FT proline or non-cysteine residue such as alanine. The variants can be used
FT for (dish)washing, as detergent additives or for fabric desizing or
FT starch liquefaction. They can also be used for the production of
FT sweeteners and ethanol from starch. See also AAW14498-99
FT
FT Sequence 478 AA;
FT
FT Query Match 100.0%; Score 40; DB 2; Length 478;
FT Best Local Similarity 100.0%; Pred. No. 19;
FT Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT QY 1 SSQDYFFH 7
FT |||||
FT 141 SSQDYFFH 147
FT
FT Db
FT
FT RESULT 7
FT AAB84206
FT ID AAB84206 standard; protein; 498 AA.
FT
FT XX
FT AC AAB84206;
FT
FT XX
FT DT 06-AUG-2001 (first entry)
FT
FT XX Amino acid sequence of a fungamyl-like alpha-amylase.
FT
FT DE Fungamyl-like alpha-amylase; glucoamylase; dextrinisation; maltose;
FT KW alcohol; starch; dough improver; brewing; starch liquification.
FT
FT XX
FT OS Aspergillus oryzae.
FT
FT XX
FT PN WO200134784-A1.
FT
FT XX
FT PD 17-MAY-2001.
FT
FT XX
FT PF 10-NOV-2000; 2000WO-DK000626.
FT
FT XX
FT PR 10-NOV-1999; 95DK-00001617.
FT
FT XX (NOVO) NOVOZYMES AS.
FT
FT PA
FT Bisgard-Frantzen H, Svendsen A, Pedersen S;
FT PI

XX WPI; 2001-367478/38.
 DR N-PSDB; AAF90208.
 XX
 PT New variant of Fungamyl-like alpha-amylase, useful for production of
 PT maltose syrups, includes mutations that improve stability against heat
 PT and acidic pH.
 XX
 PS Claim 1; Page 42-45; 49pp; English.
 XX
 CC The present sequence represents a fungamyl-like alpha-amylase. The
 CC specification describes variants of this fungamyl-like alpha-amylase,
 CC which have an alteration in one the amino acid regions 98-110, 150-160,
 CC 161-167, 280-288, 448-455, and 468-475. Each alteration is a deletion or
 CC substitution of an amino acid or an insertion of an amino acid downstream
 CC of a particular position. The variants retain alpha-amylase activity, and
 CC have better heat stability and/or stability at acidic pH, relative to
 CC wild-type enzyme. The variants can therefore be used at higher
 CC temperatures (more efficient conversion or faster reaction, and have
 CC reduced need for cooling and reduced risk of contamination). The variants
 CC may also be used in conjunction with other enzymes, particularly
 CC glucoamylase during dextrinisation. The variants are used to produce
 CC syrups, particularly of high maltose content, or alcohol, from starch; as
 CC dough improver for baked goods; in brewing, to increase fermentability of
 CC the wort; and for liquefaction of starch
 XX
 SQ Sequence 498 AA;

Query Match 100.0%; Score 40; DB 4; Length 498;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db. 161 SSQDYFH 167

RESULT 8
 ADT89632
 ID ADT89632 standard; protein; 498 AA.

XX AC ADT89632;
 XX DT 16-DEC-2004 (first entry)
 XX DE Aspergillus niger neutral alpha-amylase A (amyA) protein.
 XX KW Glucoamylase; glaA; amyA; alpha-amylase A; enzyme.
 XX OS Aspergillus niger.

XX PN US2004191864-A1.
 XX PD 30-SEP-2004.
 XX PF 31-MAR-2004; 2004US-00815495.
 XX PR 31-MAR-2003; 2003US-0459902P.
 XX PA (NOVO) NOVOZYMES BIOTECH INC.

XX PI Connelly M, Brody H;
 XX DR WPI; 2004-708545/69.
 XX DR N-PSDB; ADT89631.

XX PT Producing heterologous biological substance comprises culturing mutant of
 PT wild-type Aspergillus niger strain in medium suitable for producing
 PT heterologous biological substance and recovering heterologous biological
 PT substance.

PS Example 11; SEQ ID NO 22; 58pp; English.

XX

CC The present invention relates to a method of producing heterologous
 CC biological substance. The method involves culturing mutant of wild-type
 CC Aspergillus niger strain in medium suitable for producing heterologous
 CC biological substance, where mutant strain comprises first nucleotide
 CC sequence encoding heterologous biological substance and second nucleotide
 CC sequences comprising modification of glucoamylase (glaA) and recovering
 CC heterologous biological substance. The present sequence is the
 CC Aspergillus niger neutral alpha-amylase A (amyA) protein.
 XX
 SQ Sequence 498 AA;

Query Match 100.0%; Score 40; DB 8; Length 498;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||
 Db. 162 SSQDYFH 168

RESULT 9
 ADT89628
 ID ADT89628 standard; protein; 499 AA.

XX AC ADT89628;
 XX DT 16-DEC-2004 (first entry)
 XX DE Aspergillus niger neutral alpha-amylase B (amyB) protein.
 XX KW Glucoamylase; glaA; amyB; alpha-amylase B; enzyme.
 XX OS Aspergillus niger.

XX PN US2004191864-A1.
 XX PD 30-SEP-2004.
 XX PF 31-MAR-2004; 2004US-00815495.
 XX PR 31-MAR-2003; 2003US-0459902P.
 XX PA (NOVO) NOVOZYMES BIOTECH INC.

XX PI Connelly M, Brody H;
 XX DR WPI; 2004-708545/69.
 XX DR N-PSDB; ADT89627.

XX PT Producing heterologous biological substance comprises culturing mutant of
 PT wild-type Aspergillus niger strain in medium suitable for producing
 PT heterologous biological substance and recovering heterologous biological
 PT substance.

PS Example 10; SEQ ID NO 18; 58pp; English.

XX
 CC The present invention relates to a method of producing heterologous
 CC biological substance. The method involves culturing mutant of wild-type
 CC Aspergillus niger strain in medium suitable for producing heterologous
 CC biological substance, where mutant strain comprises first nucleotide
 CC sequence encoding heterologous biological substance and second nucleotide
 CC sequences comprising modification of glucoamylase (glaA) and recovering
 CC heterologous biological substance. The present sequence is the
 CC Aspergillus niger neutral alpha-amylase B (amyB) protein.
 XX
 SQ Sequence 499 AA;

Query Match 100.0%; Score 40; DB 8; Length 499;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSQDYFH 7
 |||||

```

Db      162 SSQDYFH 168
RESULT 10
ABP96630
ID      ABP96630 standard; protein; 1095 AA.
XX
XX
AC      ABP96630;
XX
DT      02-JUN-2003 (first entry)
XX
XX
DE      Alpha-amylase/glucoamylase fusion protein sequence SEQ ID NO:45.
XX
XX
KW      Self-processing plant; plant; processing isomerase; alpha-amylase; grain;
KW      pullulanase; alpha-glucosidase; glucose isomerase; glucoamylase;
KW      mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;
KW      maltodextrin; ethanol; fermentation; beverage; enzyme.
XX
XX
OS      Aspergillus shirousami.
OS      Synthetic.
XX
XX      WO2003018766-A2.
PN
PD
XX
XX      06-MAR-2003.
PD
PF      27-AUG-2002; 2002WO-US027129.
XX
XX
PR      27-AUG-2001; 2001US-0315281P.
XX
XX      (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
PI      Lanahan MB, Basu SS, Battie CJ, Chen W, Craig J, Kinkema M;
PI
XX
XX      WPI: 2003-268420/26.
DR
DR      N-PSDB; ACC44572.
XX
XX      Novel polynucleotide encoding hyperthermophilic processing enzymes e.g.
XX      alpha-amylase, useful for producing plant to produce food products having
XX      improved taste or fermentable substrates for ethanol.
XX
XX      Claim 1; Page 107; 158pp; English.
XX
CC      The present invention describes polynucleotides which encode processing
CC      enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
CC      isomerase, or glucoamylase) that are optimised for expression in plants.
CC      The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
CC      processing enzymes, which are activated under suitable conditions to act
CC      upon the desired substrate. Also described are self-processing transgenic
CC      plants and plant parts, e.g. grain, which express one or more of these
CC      enzymes and have an altered composition that facilitates plant and grain
CC      processing. Also described is a method (M) for converting starch to
CC      starch-derived products in a transformed plant part (TPP), by activating
CC      the starch processing enzyme contained in it. Transgenic grain is useful
CC      for preparing maltodextrin. A transformed plant (TP) can be used to
CC      produce food products having improved taste and to produce fermentable
CC      substrates for ethanol and fermented beverages. (M) eliminates the need
CC      to mill or physically disrupt the integrity of plant parts prior to
CC      recovery of starch-derived products. The present sequence represents
CC      alpha-amylase/glucoamylase fusion protein, which is given in the
CC      exemplification of the present invention
XX
XX      Sequence 1095 AA;
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Query Match      100.0%; Score 40; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 45;
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Db      141 SSQDYFH 147
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RESULT 11

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AAR88212
ID      AAR88212 standard; protein; 493 AA.
XX
XX
AC      AAR88212;
XX
DT      16-OCT-2003 (revised)
DT      03-APR-1996 (first entry)
XX
XX
DE      Alpha-amylase.
XX
XX
KW      Alpha-amylase; thermostable enzyme; baking; Aspergillus niger.
XX
XX
OS      Thermomyces lanuginosus; CBS 224.63.
XX
XX
FH      Key      Location/Qualifiers
FT      Peptide      1..18
FT      /label= Sig_peptide
XX
XX      WO9601323-A1.
PN
PD      18-JAN-1996.
XX
XX      03-JUL-1995; 95WO-EP002607.
PF
XX
XX      04-JUL-1994; 94GB-00013419.
PR
XX
XX      (DANI-) DANISCO AS.
PA
XX      Michelsen B, Rasmussen P;
PI
PI      WPI: 1996-087673/09.
DR
DR      N-PSDB; AAT10562.
XX
XX      Thermophilic alpha-amylase with activity range of 60-80 degrees C -
XX      derived from Thermomyces lanuginosus, useful in the prepn. of foodstuffs
XX      and bakery prods. esp. bread.
XX
XX      Claim 3; Page 36-38; 94pp; English.
XX
CC      A thermostable alpha-amylase (AAR88212) of Thermomyces lanuginosus CBS
CC      224.63 is expressed in Aspergillus niger hosts using a gene (AAT10562)
CC      isolated from a T. lanuginosus gene library. The recombinant enzyme (54-
CC      60 kDa) shows optimal activity at 60-70 deg and pH 5.8-6, has a pI of 3.7
CC      and is active at 60-80 deg. (Updated on 16-OCT-2003 to standardise OS
CC      field)
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XX      Sequence 493 AA;
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Best Local Similarity 85.7%; Pred. No. 76;
Matches      6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSQDYFH 7
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ID      AAO08447 standard; protein; 52 AA.
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XX
AC      AAO08447;
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XX
DT      06-NOV-2001 (first entry)
XX
XX
DE      Human polypeptide SEQ ID NO 22339.
XX
XX
KW      Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW      vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW      tissue growth factor; immunomodulatory; cancer; leukaemia;
KW      nervous system disorders; arthritis; inflammation.
XX
XX      Homo sapiens.
OS

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XX WO200164835-A2.
XX
XX
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX PF
XX 28-FEB-2000; 2000US-00515126.
XX PR
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX PA
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX DR
XX N-PSDB; AAI88378.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 22339; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 52 AA;
XX
Query Match 85.0%; Score 34; DB 4; Length 52;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SSQDYFH 7
DB 2 SSQDYMH 8
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ID AAG36453 standard; protein; 1222 AA.
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XX 18-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 44675.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
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Tue Nov 8 09:21:31 2005

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Query Match 85.0%; Score 34; DB 3; Length 1257;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1165 SSADYFH 1171

RESULT 15
AAG36451
ID AAG36451 standard; protein; 1275 AA.

XX AC AAG36451;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 44673.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
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Query Match 85.0%; Score 34; DB 3; Length 1275;

Best Local Similarity 85.7%; Pred. No. 7.9e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1183 SSADYFH 1189

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Job time : 5.09459 secs

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